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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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zf22a02.s1 Soares fetal heart NbHH19W Homo
IMAGE:377642 3', mRNA sequence.
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                                                                                                                                                                                                    Email: es@watson.wustl.edu
Email: es@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40M13 fwd. from Amersham.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA056035.1 GI:1548374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 bp mRNA linear
zf22a02.rl Soares fetal heart NbHH19W Homo sapiens
IMAGE:377642 5', mRNA sequence.
AA056035
                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 296.
                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vilson, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal heart NDH19B"
/note="Organ: heart; Vector: pT773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
/dev_stage="19 weeks"
/lab host="DHIOB (ampicillin resistant)"
/lab host="DHIOB (ampicillin resistant)"
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modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:377642"
                                                                                                                                                          /db_xref="GDB:1285898"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                    sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266
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      with RI;
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NDHL19W."

strand cDNA was primed with a Not I - oligo(dT) primer [5'

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TITLE
JOURNAL
COMMENT
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AUTHORS
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BM748818
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GluGluAlaGlnSerGlyGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim, N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-EST0023804 S9SNU601 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 1 row: C column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGAGGCCCAGAGTGGGGGAGAC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmalia; Eutheria; Primates; Catarrhin1; HOMINIOAE; HOWN. (bases 1 to 333)
m,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 333.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
/clone lib="SSNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
                                                                                                                                                                                   tissue_type="Ascites"
/cell_type="Epithelial"
/cell_tine="SNU-601"
/cell_host="Top10F'"
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                        sex="M"
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lone="S9SNU601-1-C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 bp
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Indels:
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Score:

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RESULT

US-09-017-715A-2\_COPY\_120\_127 (1-8) x BM748818 (1-333) FEATURES Query Match: REFERENCE KEYWORDS ACCESSION DEFINITION AI468480/c Best Local Similarity: Percent Similarity: Alignment Scores: AUTHORS TITLE ORGANISM JOURNAL No : : 237 GAGGAGGCCCAGAGTGGGGGAGAC 260 1 GluGluAlaGlnSerGlyGlyAsp AI468480 352 bp mRNA linear EST 30-MAR-1999 tg57g12.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:2112934 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA sequence. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 430 Std Error: 0.00 Seq primer: -40UP from Gibco Emmert-Buck, M.D., Ph.D. Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Unpublished (1997) Contact: Robert Strausberg, NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 352) Homo sapiens Homo sapiens (human) AI468480.1 GI:4330570 Email: cgapbs-r@mail.nih.gov AI468480 quality sequence stop: 323.
Location/Qualifiers Gene Index /clone lib="NCI GGAP pr28"
/clone lib="NCI GGAP pr28"
/note="Organ: prostate; Vector: pT7713D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP pr22 was prepared, and 8s
circles were made in vTtro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Patima Bonaldo. " degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pMEIBS-FL3 vector. The obtained cDNA vectors were used for transformation of compatent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library." /dev\_stage="adult" /lab\_host="DH10B" /mol\_type="mRNA" /db\_xref="taxon:9606" organism="Homo sapiens" /mol\_type="mRNA" sex="male" clone="IMAGE:2112934" 295 41.00 100.00% 100.00% 100.00% Length: Matches: Conservative: ۵ Mismatches: Indels: Ph.D. Anatomy Project (CGAP), 0000833 Sequencing Center

SOURCE

VERSION

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REFERENCE
AUTHORS
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Best Local Similarity:
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368 bp mRNA linear EST 09-OCT-2002
UI-E-CK1-afj-m-04-0-UI.81 UI-E-CK1 Homo sapiens cDNA clone
UI-E-CK1-afj-m-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
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BU729743.1
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375 Newton Road , 4156
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 368)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGluAlaGlnSerGlyGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: M13 FORWARD
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/clone_lib="UI-E-CKI"
/clone_lib="UI-E-CKI"
/notee="Organ: eye; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site_1: Site_2: Not I;
/UI-E-CKI is a normalized cDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lemnon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTCC. This library was created for the program,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="UI-E-CK1-afj-m-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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RESULT 7
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                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 484 Std Error: 0.00 Seq primer: -41m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 378)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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                                              Eye Institute (NEI).
TAG_TISSUE=Foveal and Macular Retina
TAG_LIB=UI-E-CK1
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5938504"
/db_xref="taxon:9606"
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                        (Pharmacia). Library constructed by Bento Soares and
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                                                                                                                                                                                                                                    /clone="IMAGE:726391"
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Homo sapiens cDNA clone
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Alignment Scores:

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1 (bases 1 to
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 384.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /sex="unknown"
/dev_stage="19 weeks"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHH19W"
/clone_lib="Soares_fetal_heart_NbHH19W"
/clone_lib="Soares_fetal_heart_route"
/clone_lib="Soares_fetal_heart_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_router_route
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/mol_type="mRNA"
/db_xref="GDB:1307826"
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Best Local Similarity:
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Insert Length: 484 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham.
Location/Qualifiers
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Unpublished (1997)
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Zt56h04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE.726391 5' similar to TR:G971580 G971580 SENSORY NEURON
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 484 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lab_host="DH10B (ampicillin resistant)"
clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
clone="IMAGE:726391"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="ovarian tumor"
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Indels:
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Geisel,G., Jost,S M., Martin,J.,

EST 12-AUG-1997

MO 63108

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CF529590/c
RESULT 11
AV683707
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UI-1-BClp-asy-b-08-0-UI.s1 NCI_CGAP_Pl3 Homo sapiens cDNA clone
UI-1-BClp-asy-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Ber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 404)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained Clone Distribution Soares, bento-Boares@uiowa.edu
                                                                        GAGGAGGCCCAGAGTGGGGGAGAC 298
                                                                                                      GluGluAlaGlnSerGlyGlyAsp 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="8-9 weeks"
/lab host="NH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Pl3"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site_2: Not I; NCI_CGAP_Pl3 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGAA. For additional information, contact: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_TISSUE=placenta human 8 week
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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Conservative:
Mismatches:
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 408)
                                                                                                                                                                                                                                AA946606 408 bp mRNA linear EST 23-JUL-1998 oq38c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1588630 3' similar to TR:O15104 O15104 BCSG1 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conteat: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AV683707 GKC Homo sapiens
AV683707
Unpublished (1997)
                                                                                                                                                                           AA946606.1 GI:3110001
EST.
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This clone is available
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                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anav
                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 86-21-50801919(ex.45)
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                      Tumor Gene Index
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/db_xref="taxon:9606"
/clone="GKCFPB06"
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/dev_stage="Adult"
/lab_host="SOLR"
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CDNA clone GKCFPB06 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 584 Std Error: 0.00

Seq primer: -40nil fwd. ET from Amersham.

Location/Qualifiers
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 412)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                               AI139933 412 bp mRNA linear qa68b04.xl Soares fetal heart NbHH19W Homo sapiens IMAGE:1691887 3' similar to TR:O15104 O15104 BCSG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GluGluAlaGlnSerGlyGlyAsp 8
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Insert Length: 812 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 359.
Location/Qualifiers
                                                                                                                                         Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                       AI139933.1 GI:3647390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAGGCCCAGAGTGGGGGAGAC 286
                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1588630"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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AUTHORS
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AV703171
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ORGANISM
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ACCESSION
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                                                                                                                                                             FEATURES
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                          Fax: 86-21-50801922
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lone is available at CHGC in
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1691887"
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                                                                                                             organism="Homo sapiens"
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'clone_lib="ADB"
'note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                  tissue_
                                                                                  clone="ADBBCF03"
                                                                                                 db xref="taxon:9606"
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                                                                  type="Adrenal gland"
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Pred. No.:
                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 428)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX090816 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE998F081781; IMAGE:726391, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RZPD; IMAGD998P081781.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Ina Rolfs
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                                                                                                     M.Fatima Bonaldo.
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/db_xref="taxon:9606"
/clone="IMAGD998P081781 ; IMAGE:726391"
                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                            Pharmacia).
                                                                                                                                                                                                                                                                          tissue_type="ovarian tumor"
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Search completed: May 4, 2005, 13:46:36 Job time: 364.973 secs

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Result
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-MODBLE frame + D21 model - DEV=x1h
-Q-/cgn2 1/USPTO spool h/US99017715/runat 04052005 100744 25619/app_query.fasta_1.661
-Q-/cgn2 1/USPTO spool h/US99017715/runat 04052005 100744 25619/app_query.fasta_1.661
-DB=EST -QFWT=fastap - SUFFIX_FSt - MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -ENDE-1 -MATRIX=biosum62 -TRANS=hunan40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US99017715 @CGN 1 5334 @Tunat 04052005 100744 25619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DS9BLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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         4 C W 4 D D C B P
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UI-E-CK1-
K-EST0023
AV708398
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7 zt56h04.r
7 AV683707
8 qa68b04.x
L AV703171
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AUTHORS
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BE774132
BE774132.1
EST.
                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 161)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Nara M. T., Goard P. Parentri B. B. Parentri B. B. Coura G. T. and O'Nara M. T. Goard P. P., Jongeneel, C.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                            Fax: +55-11-2707001
                                                                Tel: +55-11-2704922
                                                                                                                                                                                                                            Proc. Natl. Acad.
20202663
                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                             Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                  O'Hare, M.J., Soares, F., Brentani, R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MR1-UM0009-220500-015-g07_1 UM0009
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AIR84600
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BG826435
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UI-E-CQ1.

UI-E-CQ1.

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RESULT 2
BM693306
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Best Local Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                       Coordinated Laboratory for University of Iowa 375 Newton Road , 4156 Prel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 bp mRNA linear EST 28 UI-E-CK1-afm-i-14-0-UI.rl UI-E-CK1 Homo sapiens cDNA clone UI-E-CK1-afm-i-14-0-UI 5', mRNA sequence.
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Seq primer: puc 18 forward
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Location/Qualifiers
                                                                                                                                                            Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8889548
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                                                                                                                  Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
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                                                                                                                                           Genetics (www.resgen.com).
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                                                                                          primer: M13 Reverse.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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mol_type="mRNA"
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ne_lib="UM0009"
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Indels:
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RESULT 3
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Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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Genome Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-EST0023804 S9SNU601 Homo sapiens cDNA clone S9SNU601-1-C11 5',
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                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 1 row: C column: 11
                                                                                                                                                                                                                                                                                                           52 Eoeun-dong Yuseong-gu,
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM748818.1 GI:19078436
                                                                                                                                                                                                                                                                                          Fax: +82-42-860-4409
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                                                                                                                                                                                                                quality sequence stop:
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UI-E-CK1 is a normalized CDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT773-pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GTCC. This library was created for the program,
Gene Discovery in the Visual System, supported by National
Eye Institute (NEI)."
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CK1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
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/db_xref="taxon:9606"
                                                                                                                                                                                            Location/Qualifiers
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                                              /sex="M"
                                                                         clone="S9SNU601-1-C11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="UI-E-CK1-afm-i-14-0-UI"
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Matches:
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Indels:
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Kim,J.M., Park,H.S., Kim,S. and
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Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV708398 ADC Homo sapiens
AV708398
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                                                                                                                                                                                                                                                                                                                         This clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCAACAG 200
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//note="forgan: Stomach; Vector: pME18-FL3; Site_1: XhoI;
/inote="forgan: Stomach; Vector: pME18-FL3; Site_1: XhoI;
Site_2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Sfil
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using Sfil
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with Sfil and
cloned into DraIII- digested pME18S-FL3 vector. The
obtained cDNA vectors were used for transformation of
compsetent cells E. coli ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
                                                                                                                                                                                                                                                                                         e is available at CHGC in Shanghai.
Location/Qualifiers
note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                /tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                  /db_xref="taxon:9606"
/clone="ADCAMB05"
                                                                                                                                                                                                    organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="Top10F'"
/clone_lib="S9SNU601"
                                        clone lib="ADC"
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                                                 Alignment Scores:
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                                   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 bp mRNA linear zg83h10.s1 Soares_fetal_heart_NbHH19W Homo sapiens IMAGE:400003 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 384.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 387)
                                                                                                /mol_type="mRNA"
/db_xref="GDB:1307826"
                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                       dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                         sex="unknown
                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:400003"
                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9606"
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CDNA clone
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AA394097
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                                         US-09-017-715A-2_COPY_94_107 (1-14)
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Kucaba,T., Lacy,M., Le,N., Lemnon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zt56h04.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:726391 5' similar to TR:G971580 G971580 SENSORY NEURON A394097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 484 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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                ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5938504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
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/clone="IMAGE:726391"
                                                                                                                                                                                                                                  Pharmacia).
                                                                                                                                                                                                                                                                                                                                                                                                        sex="Female"
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                                      SOURCE
                                                                     VERSION
                                                                                   ACCESSION
                                                                                                                                       DEFINITION
                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                  US-09-017-715A-2_COPY_94_107 (1-14) x AV683707 (1-407)
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                                                                                                                                                                    AI139933/c
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                                                                                                                                                        Focus
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MEDLINE
                    ORGANISM
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                                                                                     sequence.
                                                                                                                  AII39933 412 bp mRNA linear qa68b04.x1 Soares fetal heart NbHH19W Homo sapiens IMAGE:1691887 3' similar to TR:015104 O15104 BCSG1
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AV683707
                                                                                                                                                                                                                       1 (bases 1 to 407)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 86-21-50801919(ex.45)
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                                                                     AI139933.1 GI:3647390
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                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hepatocellular
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/acl_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GKC"
/note="Vector: pBluescript sk(-);    Site_1: EcoRI;    Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="GKCFPB06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:9606"
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Road, Zhangjiang Hi-Tech Park,
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma"
                                                                                                                                                                                                                                                                                                                        linear EST 16-JAN-2
306 5', mRNA sequence.
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                                                                                                                    EST 05-OCT-1998 cDNA clone PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 16-JAN-2002
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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AV703171
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Query Match:
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                      Induity of the Control of the Contro
                                                                                                                                                                                                Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., Chen,Z. and Han,Z. Homo sapiens CDNA ADB clones
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AV703171 ADB Homo sapies
AV703171
AV703171.1 GI:10720500
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 584 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Unpublished (1997)
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1 (bases 1 to 412)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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86-21-50801919(ex.45)
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/db_xref="taxon:9606"
/clone="IMAGE:1691887"
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Matches:
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BX090816
LOCUS
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DB:
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Best Local Similarity:
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                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                                                                                                                                                                                         This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human UnigeneSet -
Unpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 428)
Ebert, L., Heil, O., Hennig, S., Neubert, P.,
Radelof, U., Schneider, D. and Korn, B.
                                                                                                                                                                                                                                                       www.rzpd.de
                                                                                                                                                                                                                                                                              Tel: +49 30 32639
Fax: +49 30 32639
                                                                                                                                                                                                                                                                                                                   http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rc
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rc
RZPD Deuteches Ressourcenzentrum fuer Genomforschung
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                   RZPD; IMAGP998P081781.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX090816 428 bp mRNA linear EST 23-JAN-2003 BX090816 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGD:98P081781 ; IMAGE:726391, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 86-21-50801922
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clone is available at CHGC in Shanghai.
                                                           /organism="Homo sapiens"
/mal_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGp998P081781 ; IMAGE:726391"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                            sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Adrenal
/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="ADBBCF03"
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                           Ina Rolfs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI684600 438 bp mRNA linear EST 07-MAR-200 wa84d12.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2302871 3' similar to TR:015104 O15104 BCSG1 PROTEIN. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 505 Std Error: 0.00 Seg primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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                                                                        /clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker, Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687339,
726408-728711, and 729096-7319. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2302871"
/lab_host="DH10B"
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RESULT 13
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AUTHORS
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Best Local Similarity:
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mRNA sequence.
BG826435
BG826435.1 GI:
EST.
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442 bp mRNA linear EST 19-FEB-1998
of44b01.sl NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1427017 3'
similar to SW:SYUN_RAT Q63544 SENSORY NEURON SYNUCLEIN. ;, mRNA
                                            Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 795 Std Erro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 301.
                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCI CGAP_CNS1"
/note="Organ: brain; Vector: pCMV-SPORT4; Site_1: Sall;
Site_2: Noti; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.0 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
/mol_type="mRNA"
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lone="IMAGE:1427017"
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                                                                                                                                                                                                                                                                                     462 bp mRNA
DKF2p686E24170 r1 686 (synonym: hlcc3) F
DKF2p686E24170 5', mRNA sequence.
BX474511
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                                                                       Fobo,G., Han,M. and Wiemann,S.

EST (Bloecker,H., Boecher,M., Mewes,H.W.,
Unpublished (2003)
                                                                                                                                                  Mammalia; Eutheria;
1 (bases 1 to 462)
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                 Homo
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Ingolstaedter Landstr.1, D-85764 Neuherberg, This is the 5' sequence of the clone insert
                                                           Contact: MIPS
                                                                                                                                  Bloecker, H.,
                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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High quality sequence stop: 447.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G): Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4903046"
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Matches:
Conservative:
Mismatches:
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                                                                                             Weil, B.,
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                                                                                                                                  Amid, C., Osanger, A.,
                                                                                             Amid, C.,
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                                                                                              et al.)
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JOURNAL
COMMENT
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CB107161
LOCUS
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SOURCE
                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                      source
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US-09-017-715A-2_COPY_94_107 (1-14) x
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                   Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 467)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                                                                                                                                                                                                                                 Email: yongsung@mail.kribb.re.kr
Plate: 14 row: A column: 11
                                                                                                                                                                                                                                                                                    Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                              Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                       21C Frontier Korean EST Project 2001 Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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CB107161.1 GI:27932968
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Location/Qualifiers
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This clone (DKFZp686E24170) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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                                                                                                                                                                                                           quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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note="Vector: pTriplEx2; Site_l: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligate and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligates after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

US-09-017-715A-2_	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
COPY_94_107	0.0537 70.00 70.00% 100.00% rity: 100.00% 6
/ (1-14) x (	000 000 000 000
CB107161 (1-	Length: Matches: Conservative: Mismatches: Indels: Gaps:
467)	467 14 e: 0 0
	US-09-017-715A-2_COPY_94_107 (1-14) x CB107161 (1-467)

Search completed: May 4, 2005, 13:46:35 Job time: 639.953 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5642217 seqs, 3043843248 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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748.404 Million cell updates/sec
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SUMMARIES

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Sequence 37660, A	eduction of or	47650	9722, I	Sequence 9553, Ap	, ,	e 52591,	967	0000	0 0 0 0 0 0	· 118	ı. Ar	262,	e 17537	_	e 28635	e 2	e 255	e 1012	e 10	e 10123	e 1012	6012,	e 14192	e 16587	e 236	e 1, Appl	e 1, Ap	e 483,	e 483,	e 73,	e 72,	e 73,	e 72, 7	e 388,	Sequence 172,	quence 172,	Sequence 1	quence 171,	equence 469,	equence 469,	equence 297, i	Sequence 1680, Ap	1, Ap	613, Ap	Sequence 2705, Ap	quence 5, Ap	

## ALIGNMENTS

RESULT 1 US-10-826-157-5

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CURRENT APPLICATION NUMBER: US/10/826,157;
CURRENT FILING DATE: 2004-04-16;
PRIOR APPLICATION NUMBER: US 60/472,317;
PRIOR FILING DATE: 2003-05-20;
PRIOR APPLICATION NUMBER: US 60/463,284;
PRIOR FILING DATE: 2003-04-16;
NUMBER OF SEQ ID NOS: 8;
SOFTWARE: FASISEQ for Windows Version 4.0;
SEQ ID NO 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10826157
Publication No. US20050064548A1
                                                                                                                                                                                                                                                                                                 APPLICANT: Lindquist, Susan L.
APPLICANT: Outeiro, Tiago
TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
FILE REFERENCE: 17481-003001
Q ID NO 5
LENGTH: 384
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; TYPE: DNA
; ORGANISM: Ho
US-10-826-157-5
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Best Local Similarity:
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                                                                                                                                                                                                                                              Sequence 613, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2705
LENGTH: 479
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APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(479)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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on No. US20030073623A1
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Conservative:
Mismatches:
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Percent Similarity:
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; ORGANISM: Homo
US-09-954-531-613
; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-453-478-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: US/
                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
                                      TOPOLOGY: lin
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 II
COMPUTER: IBM PS/2
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                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/705,771 FILING DATE: August 30, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ROSELAND
STATE: NEW JERSEY
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CECCHI, STEWART
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                                                                                                            LENGTH: 550 base pairs
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APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 68920-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-66-05
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR APPLICATION NUMBER: US/09/962,832
US-10-097-340-297; Sequence 297, Application US/10097340; Publication No. US20030087250A1
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                                                                RESULT 6
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US-10-843-641A-1680
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-10-03
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-09-28
APPLICATION NUMBER: US/09/968,007
FILING DATE: 2001-10-02
APPLICATION NUMBER: US/09/969,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/964,824 FILING DATE: 2001-09-27
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APPLICATION NUMBER: US/09/969,708
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                                                                                                                        GTGGTGCGCAAGGACTTGAGGCCATCTGCCCCCCAACAG 332
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Indels:
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/314,967
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
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Best Local Similarity:
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                                                                                                                                                                                  Sequence 469, Application US/10282174
Publication No. US20030224380A1
GENERAL INFORMATION:
APPLICANT: Becker, Kenneth David
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NUMBER OF SEQ ID NOS: 363
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                                            APPLICANT:
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PRIOR APPLICATION NUMBER: 60/323,580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
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Tanzi, Rudolph E.
Bertram, Lars
Saunders, Aleister J.
Mullin, Kristina M.
Sampson, Andrew Johnson
Blacker, Deborah Lynne
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                                                                       Elliot, Ka
Wang, Xin
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Ami SEN
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Karen GLATT
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Robert C. BAST, Jr.
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Best Local Similarity:
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PRIOR FILLING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILLING DATE: 2001-11-08
PRIOR FILLING DATE: 2001-11-08
PRIOR FILLING DATE: 2001-11-08
PRIOR FILLING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR FILLING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILLING DATE: 2001-12-04
PRIOR FILLING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
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SEQ ID NO 469
LENGTH: 720
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TITLE OF INVENTION: GENES AND POLYMORPHISMS ON C
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
FILE REFERENCE: 37481-3308B
CURRENT APPLICATION NUMBER: US/10/600,009
CURRENT FILING DATE: 2003-06-18
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
                 PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILLING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILLING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR FILLING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR APPLICATION NUMBER: US 60/338,363
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APPLICANT: Velicelebi, Gonul
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NAME/KEY: allele
LOCATION: 30,57,85,243,250,377,512,531,555,561,672
OTHER INFORMATION: N is any
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CURRENT FILING DATE: 2002-10-25
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TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
THE REFERENCE: 37481-3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469,
                                                                                                                                                                                                                                                                               I: Sampson, Andrew Johnson
I: Blacker, Deborah Lynne
INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
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                                                                                                                                                                                                                                                                                                                                                                                                                            Bertram, Lars
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Tanzi, Rudolph E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elliot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10600009
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Indels:
Gaps:
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PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR PELICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/282,174
PRIOR FILING DATE: 2002-10-25
PRIOR FILING DATE: 2002-10-25
PRIOR FILING DATE: 2002-10-25
PRIOR FILING DATE: 564
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 469
LENGTH: 720
RESULT 10
US-10-102-806-171
; Sequence 171, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                              US-09-017-715A-2_COPY_94_107 (1-14) x US-09-925-298-171 (1-796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 171, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 171
LENGTH: 796
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 30,57,85,243,250,377,512,531,555,561,672
OTHER INFORMATION: N is any
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                               388
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                                                                                                              GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 429
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Matches:
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Matches:
Conservative:
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RESULT 12
US-10-102-806-172
Sequence 172, Application US/10102806
; Publication No. US20030054421A1
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Best Local Similarity:
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Best Local Similarity:
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 172, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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TYPE: DNA
ORGANISM: Homo sapiens
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70.00
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Matches:
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Sequence 388, Application US/10240425

Publication No. US20040033502A1

GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Williams, Amanda
APPLICANT: Lord, Reginald V.
APPLICANT: Lord, Reginald V.
APPLICANT: Verzel, Jon C.
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026

CURRENT APPLICATION NUMBER: US/10/240,425

CURRENT APPLICATION NUMBER: PCT/US01/09847

PRIOR APPLICATION NUMBER: PCT/US01/09847

PRIOR APPLICATION NUMBER: US 60/193,446

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2000-03-31

NUMBER: Patentin Ver. 2.1

SEQ ID NO 388

LENGTH: 4606
                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                  Alignment Scores:
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Query Match:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-806-172
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
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SEQ ID NO 172
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                              LENGTH: 4606
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 112
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Matches:
Conservative:
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Indels:
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Conservative:
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US-09-017-715A-2\_COPY\_94\_107 (1-14) x US-10-240-425-388 (1-4606)

3950 CAGGAGGACTTGAGGCCATCTGCCCCCAACAG 3982

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US-09-017-715A-2_COPY_94_107 (1-14) x US-10-282-174-72 (1-5666)
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Best Local Similarity:
Query Match:
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US-10-282-174-72
                                                                                                                                                                                                                                                                                     RESULT 15
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PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR PPLICATION NUMBER: US 60/338,363
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 5666
                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                         Sequence 73, Application US/10282174 Publication No. US20030224380A1
                                                                                                              APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
                                                                          APPLICANT:
                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Becker, Kenneth David
    APPLICANT:
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 37481-3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                4512 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 4544
                                                                                                                                                                                                                                                                                                                                                               4 LysGluAspLeuArgProSerAlaProGlnGln 14
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No. US20030224380A1
Bertram, Lars
Saunders, Aleister J.
Mullin, Kristina M.
                                                                     Wang, Xin
Tanzi, Rudolph E.
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75.71%
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Indels:
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Job time : 126.546 secs

Search completed: May 4, 2005, 16:39:43

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PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-03-28
PRIOR FILING DATE: 2002-03
B
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                          US-09-017-715A-2_COPY_94_107 (1-14) x US-10-282-174-73 (1-5666)
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TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: MURDERENERATIVE DISEASES
FILE REFERENCE: 37481-3308
CURRENT APPLICATION NUMBER: US/10/282,174
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-10-25
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APPLICANT:
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NAME/KEY: allele
NAME/KEY: 3779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/338,010 PRIOR FILING DATE: 2001-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 4976
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
NAME/KEY: allele
LOCATION: 560,590,617,645,915,987,1723,1943,1950,3151,3178,3189,3284,
LOCATION: 4276,4311,4552,4995,5019,5025,5112,5136,5421,5648,5517
OTHER INFORMATION: N is any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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4512 CAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 4544
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100.00%
90.91%
75.71%
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Matches:
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Indels:
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Result
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Maximum
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Maximum Match 100%
Listing first 45 s
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-QQ-/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100745_25632/app_query.fasta_1.661
-QQ-/cgn2_1/USPTO_spool_h/US09017715/runat_04052005_100745_25632/app_query.fasta_1.661
-DB=1Bsued_patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite -STRATE1 -END=-1 -MATKIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-USER=US09017715_0CGN 1 1 116 @runat_04052005_100745_25632 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      length: 0
length: 2000000000
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Match
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Ygapop 10.0 , X
Fgapop 6.0 , E
Delop 6.0 , E
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                                                                                                                                                                                                               BB
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Ygapext
Fgapext
Delext
US-08-705-771-1
US-09-417-540-1
US-09-949-016-1915
US-09-949-016-12164
US-09-949-016-12184
US-09-949-016-12184
US-09-103-840A-2
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US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-2
US-09-103-840A-2
US-09-103-840A-3
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706.682 Million cell updates/sec
                               Sequence 1, Appli
Sequence 1, Appli
Sequence 1915, Ap
Sequence 1915, Ap
Sequence 13657, A
Sequence 12184, A
Sequence 172, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 8804, Ap
                                                                                                                                                                                                            Description
                  Appli
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Sequence 1, Application.

Sequence 1, Application.

Patent No. 6054289

Patent No. 6054289

GENERAL INFORMATION

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,

APPLICANT: Jian Ni and Jing-Shan Hu

ITILE OF INVENTION: Human Genes, Sequences and

ITILE OF INVENTION: Expression Products

TITLE OF INVENTION: Expression Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-705-771-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
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                                              APPLICATION NUMBER: US/08/705
PILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
   TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILLADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                        COUNTRY:
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N: 536
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US-09-949-016-17185
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US-09-949-016-115274
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US-09-949-016-115274
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US-09-280-116-13287
US-09-281-19-9
US-09-443-795-2
US-09-949-016-135661
US-09-949-016-13661
US-09-949-016-15663
                                                                                  325800-346 (PF196)
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US-09-419-568F-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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13161, 15660, 15661, 15662,

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5443, Appl 24, Appl 24, Appl 25, Appl 25, Appl 1659, Ap 1659, Ap 1662, Ap 1062, Ap 114544, 1446, Appl 1476, App

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LENGTH:

: 550 base pairs nucleic acid

single

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Best Local Similarity:
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                                        score:
                                                                         Alignment Scores:
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                                                                                                                US-09-417-540-1
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: si
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTMARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,540
FILING DATE: 14-Oct-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                              MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji, Jian Ni and Jing-Shan Hu TITLE OF INVENTION: Human Genes, Sequences and Expression Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 332
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                                                                                                                                                                                LENGTH: 550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
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                   Length:
Matches:
Conservative:
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Matches:
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Indels:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANY: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ETLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SEQ ID NO 42
LENGTH: 720
TYPE: NYA
THERESE OF SET MINDOWS Version 4.0
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DB:
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-442
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Patent No. 6812339
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Patent No. 6812339
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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Query Match:
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US-09-949-016-13657
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13657
                                                                                                                                                                                                      Sequence 12184, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Patent No. 6812339
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TYPE: DNA
ORGANISM: Human
FEATURE:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
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LOCATION: (1)...(8607)
OTHER INFORMATION: n =
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Matches:
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Matches:
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OF DETECTION AND USES THEREOF
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RESULT 8
US-09-103-840A-2/c
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DB:
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Best Local Similarity:
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-172
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        Sequence 2, Application US/09103840A
Patent NO. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 172
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12184
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TYPE: DNA
ORGANISM: Human
FILE REFERENCE: 24366-20007.00
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NAME/KEY: misc_feature
LOCATION: (1)...(8608)
OTHER INFORMATION: n = A,T,C
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Indels:
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; Sequence 8804, Application U; Patent No. 6833447; GENERAL INFORMATION: APPLICANT: Goldman, Barry S; APPLICANT: Hinkle, Gregory; APPLICANT: Slater, Steven
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                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                                                                               US-09-902-540-8804
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CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA SEQUENCES FOR STRAITITE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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OTHER INFORMATION:
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Best Local Similarity:
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 Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 bass
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LENGTH: 1011
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TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                                                                                                                                                                                                                                                 NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/00
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                   STRANDEDNESS: BITTOPOLOGY: linear
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MATERIALS AND METHODS FOR PRODUCING
PLANTS WITH SINGLE-SEX FLOWERS
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Percent Similarity:
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Query Match:
                                                                                                        CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                    PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5443
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5443, Appendix No. 681233
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SEQ ID NO 935
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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LOCATION: (1)..(10096)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Human
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Best Local Similarity:
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                                                                                                                              APPLICANT: Dumoutier,
APPLICANT: Louhed, Ja
APPLICANT: Renauld, J
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                        Sequence 24, Application US/09354243B Patent No. 6359117 GENERAL INFORMATION:
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No. 6331617
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Patent No. 6331.
Patent No. 6331.
Patent No. 6331.
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
EQ ID NO 24
                                                                        FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fact
TITLE OF INVENTION: (TIFs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/419,568F CURRENT FILING DATE: 1999-10-18
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 690
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Renauld, Jean-Christophe
Renauld, Jean-Christophe
RENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
                                                                                                                                                                                                                                     Dumoutier, Laure
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                                                                                                                                          Uses Thereof
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; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
US-09-354-243B-24

Alignment Scores: 156
Pred. No.: 42.00
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 80.00% Matches: 1
Best Local Similarity: 80.00% Indels: 0
DB: 3
COPP-94_107 (1-14) x US-09-354-243B-24 (1-690)

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-354-243B-24 (1-690)

US-09-017-715A-2_COPY_94_107 (1-14) x US-09-354-243B-24 (1-690)

Search completed: May 4, 2005, 09:42:48

Search completed: May 4, 2005, 09:42:48
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Result
No.
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-Q=/Cgn2 1/USPTO spool h/US09017715/runat 04052005 100743 25600/app query.fasta_1.661
-Q=/Cgn2 1/USPTO spool h/US09017715/runat 04052005 100743 25600/app query.fasta_1.661
-DB=N Geneseg -QFMT=fastap -SUPTIX=run -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -STNART=1 -ENDS-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=US09017715_@CGN 1 _703_@runat_04052005_100743_25600 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONCLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOD=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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 ACH15493
ADM66887
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ABL63343
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Ach15493 Human adu
Adm66887 Human hom
Aav42669 Human bre
Aaa39470 Human HBG
Ab163343 Breast ca
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## ALIGNMENTS

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RESULT 1
ACH15493
ID ACH15493 standard; cDNA; 479 BP.

XX
AC ACH15493;
XX
AC ACH15493;
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DT 13-OCT-2003 (first entry)
XX
DE Human adult brain cDNA #2705.
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DE Human adult b
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US-09-017-715A-2_COPY_94_107
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                             human; adipocyte specific; gene; ds; adipose tissue; anti-obesity; high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes; adipogenesis; hypertension; cardiovascular disease; anorectic; antidiabetic; hypotensive; gamma synuclein.
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                                                             29-JUL-2002; 2002US-0398785P
12-JUN-2003; 2003US-0478206P
                                                                                                                        29-JUL-2003; 2003WO-US023684
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                                                                                                                                                                                                                                                                                                                                                                                    Human homologue of
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                         (HMGE-) HMGENE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for identifying genes that are cover-expressed in adipose tissue and as such it provides targets for antice cobesity pharmaceutical compositions. Specifically, it refers to a high combility group I-C protein (HMGI-C) that is associated with obesity and combility group I-C protein (HMGI-C) that is associated with obesity and combility group I-C protein (HMGI-C) that is associated with obesity and combility group I-C protein (HMGI-C) that is associated with obesity and composition describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) compounds that are adipose tissue (WAT) or stromal vascular tissue (SVT) compounds that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity. These compositions exhibit anorectic, antidabetes or obesity. These compositions exhibit anorectic, antidabetes and human homologue of a murine adipocyte specific DNA sequence is a human homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue mice of different genotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 488
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                                                                                                                                                                                                                      Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis; therapy; genetic marker; ds.
                                                                                                                                                                                                                                                                  Human breast cancer specific gene 1 (BCSG1) cDNA
                                                                                                                                                                                                                                                                                                  09-NOV-1998
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                                                                                                                                                                                                                    therapy;
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                                                                                                                                                                                                                  genetic
                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGTGCGCAAGGACTTGAGGCCATCTGCCCCCCAACAG 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                        /*tag=
                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 176
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Matches:
Conservative:
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Indels:
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03-FEB-1997; 03-FEB-1998;

97US-0037080P 98WO-US001804.

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RESULT 4

AAA39470

ID AAA3

XX AAA3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone corresponds to the transcript of the newly identified CD human breast cancer specific gene 1 (8CSG1), and includes an open reading frame for a 14.2 kDa protein (see AMAG3123). It was isolated from a breast cancer cDNA library following an EST search for novel genes consisted at ATCC 97175 and ATCC 97885. A gradient and stage specific BCSG1 expression has been demonstrated from virtually no consisted expression in has been demonstrated from virtually no consisted expression in normal or benign breast to low level and partial expression in low grade in situ breast carcinoma and high expression in consistency in the filtrating malignant breast carcinomas. BCSG1 is useful as a breast cancer progression marker. Recombinant vectors and host cells useful for recombinant production of BCSG1 polypeptides (including epitope-bearing polypeptides) are provided. BCSG1 polypeptides, polypeptides and cantibodies can be used for the detection of breast cancer calls or breast cancer metastasis, and to develop methods for the clinical management and treatment of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                Human; ADA2;
amyloid-like
                             30-AUG-1996;
                                                                                     25-APR-2000.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HBGBA67A DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-446811/38.
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                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gene therapy; treatment; cancer; protein; ss.
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                             96US-00705771
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                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                /product= "HBGBA67"
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Best Local Similarity: Query Match:
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20-SEP-2000;

20-SEP-2000;

20-SEP-2000;

22-SEP-2000;

22-SEP-2000;

25-SEP-2000;

25-SEP-2000;

25-SEP-2000;
                                                                                                           05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                  Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                05-JUN-2000;
                                                                                                                                                                        30-MAY-2001;
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                    Breast cancer related gene sequence SEQ ID NO:1680.
                                                                                                                                                                                                                                                                                                                                                                                                              ABL63343 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 550 BP; 132 A; 145 C; 192 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel polynucleotide (I) encoding human ADA2. The products of the invention have cytostatic activity and can be used for gene therapy. (I) is useful for testing cancer; as primers and probes for isolating full length cDNA and genes having similar biological activity. This sequence encodes a polypeptide derived from the human HBGBA67X clone which is an amyloid-like protein found in breast tissue
                                                                                                                                                                                                                                                                                                                                                              15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-338491/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 GTGGTGCGCAAGGACGTTGAGGCCATCTGCCCCCCAACAG 332
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2000US-0234009P.
2000US-0234034P.
2000US-0234052P.
2000US-0234509P.
2000US-0234567P.
2000US-0234923P.
2000US-0234923P.
2000US-0235077P.
2000US-0235082P.
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2000US-0233133P.
2000US-0233617P.
                                                                                                                                                                         2001WO-US010838.
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02-OCT-2000;
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02-OCT-2000;
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28-SEP-2000
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28-SEP-2000
29-SEP-2000
02-OCT-2000
02-OCT-2000
                                                                                                                                                                                       (AVAL-) AVALON PHARM
                                                                                                                                                                                                                         2000US-0235711P.
2000US-0235720P.
2000US-0235843P.
2000US-0235863P.
2000US-0236038P.
2000US-0236034P.
2000US-0236111P.
2000US-0236111P.
2000US-0236111P.
2000US-0236112P.
2000US-0236172P.
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2000US-0235280P.
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PE, Augustus M, Weaver Z; Carter č, Ebner R, Endress Ó Horrigan

WPI; 2002-188264/24.

Screening reening for anti-neoplastic agent involves exposing cells to ent to be tested for anti-neoplastic activity, and determining expression of a gene of a signature gene set. osing cells to a chemical and determining a change

Claim 1; SEQ ID NO 1680; 44pp; English.

The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AB161664 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, obsophageal, ovarian, kidney, protected or reportation and clear cell prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squ cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wi oular cancer, squamous carcinoma and Wilm's

Sequence 550 BP; 132 A; 145 Ç 192 G; 81 <del>, ,</del> 0 U; 0 Other;

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Percent Similarity:
Best Local Similarity:
                                    Pred.
                                          Alignment
      Query Match:
                                    No.:
      0.00526
70.00
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100.00%
      Mismatches:
Indels:
Gaps:
                    Matches:
Conservative:
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US-09-017-715A-2\_COPY\_94\_107 (1-14) × ABL63343 (1-550)

Sequence 550 BP; 132 A; 145 C; 192 G;

81

₽, 0

U; 0 Other

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ARESULT 6
ARWT3813
ID W73813
ID W738
                                                                                                                                                                                                                                                                                                                                       The present sequence is that of cDNA encoding the Glu-110 isoform of human gamma-synuclein. The invention relates to an isoform of gamma-synuclein that is caused by an A/T single nucleotide polymorphism (SNP) at position 329 of the gamma-synuclein coding sequence. This SNP causes glutamic acid to valine change at amino acid position 110 of gamma-synuclein, and is associated with an increased susceptibility of individuals to schizophrenia spectrum disorders (SSDs). This is the first that a genetic component of SSDs has been identified, and provides potential target for diagnosis and treatment of schizophrenia. Gamma-synuclein polypeptides, especially those containing the E110V mutation, are used in a claimed method of screening for compounds useful for the
                                                                                  treatment of SSDs, and gamma-synuclein expressing cells are used in a claimed method of screening for agonist or antagonist compounds. An oligonucleotide complementary to part of the gamma-synuclein coding sequence is used for the discrimination of an SNP at position 329 of the coding sequence. Gamma-synuclein polypeptides or polynucleotides are also useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR amplification of a polynucleotide encoding gamma-synuclein and analysis of the occurrence of the SNP at position 329. A transgenic animal useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gamma-synuclein; human; single nucleotide polymorphism; SNP;
schizophrenia; neuroleptic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for compounds for treating or interfering with the onset of Schizophrenia Spectrum Disorders, by detecting interactions of candid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compounds with the gamma-synuclein polypeptide.
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NOVARTIS-ERFINDUNGEN VERW GES
UNIV MARYLAND BALTIMORE.
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synuclein that is caused by an A/T single nucleotide polymorphism (SNP) at position 329 of the gamma-synuclein coding sequence. This SNP causes a glutamic acid to valine change at amino acid position 110 of gamma-synuclein, and is associated with an increased susceptibility of individuals to schizophrenia spectrum disorders (SSDs). This is the first time that a genetic component of SDs has been identified, and provides a potential target for diagnosis and treatment of schizophrenia. Gammasynuclein polypeptides, especially those containing the EllOV mutation, are used in a claimed method of screening for compounds useful for the
                                                                                                                                                                                                                                                                                                                                                                                                      Screening for compounds for treating or interfering with the onset of Schizophrenia Spectrum Disorders, by detecting interactions of candidate compounds with the gamma-synuclein polypeptide.
                                                                                                                                                                                                                                                                The present sequence is that of cDNA encoding the Val-110 isoform of human gamma-synuclein. The invention relates to an isoform of gamma-
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schizophrenia; neuroleptic; mutant; gene;
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page; 32pp; English.
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The invention relates to isolated new isolated protein and nucleic acid molecules useful for diagnostic and therapeutic purposes. The invention is for treating genetic diseases such as muscular dystrophy or cystic

New isolated protein and nucleic acid molecules, useful for diagnostic and therapeutic purposes, e.g. for treating genetic diseases such as muscular dystrophy or cystic fibrosis.

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Fig 1; Opp; English.

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30-AUG-1996;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrosis, and for in
synthesis of DNA and
in gene therapy. The
             The invention relates to an isolated human polypeptide. The polypeptides, polynucleotides, agonists or antagonist are useful for diagnosing or treating genetic diseases such as muscular dystrophy or cystic fibrosis, hypertension, angina pectoris, myocardial infarction, ulcers, asthma, allergies, psychoses, depression, migraine, vomiting, benign prostatic hypertrophy or osteoporosis. The polypeptides and polynucleotides are useful for in vitro purposes related to scientific research, synthesis of
                                                                                                                                                                                                                                                                                                                                                  04-JUN-2003; 2003US-00453478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; gene; muscular dystrophy; cystic fibrosis; hypertension;
angina pectoris; myocardial infarction; ulcer; asthma; allergy;
psychosis; depression; migraine; vomiting; benign prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human amyloid like
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                                                                                                                     Claim 18; SEQ ID NO 1; 56pp; English.
                                                                                                                                               hypertension,
                                                                                                                                                         New human polypeptides and polynucleotides, useful for diagnosing or treating genetic diseases such as muscular dystrophy or cystic fibrosis,
                                                                                                                                                                                                                                           Moore PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis;
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                                                                                                                                                                                                                2003-864796/80.
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    manufacture
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                                                                                                                                                                                                                                           Gentz RL,
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                                                                                                                                             asthma, depression or osteoporosis.
                                                                                                                                                                                                                                                                                             95US-0002993P.
96US-00705771.
99US-00417540.
                                                                                                                                                                                                                                                                     GENOME
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/product= "Amyloid like protein"
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  purposes related of DNA vector. T
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Matches:
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  sequence represents cDNA
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RESULT 10
AAX29997
                                                   Percent Similarity:
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Query Match:
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                            US-09-017-715A-2_COPY_94_107 (1-14) x AAX29997 (1-720)
                                                                                            Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding human amyloid like protein.
                                                                                                                                                                This sequence represents the gene encoding a novel human synuclein family member designated persyn. The sequence is useful for screening, diagnosing or monitoring cancer (especially breast or skin cancer), neurodegenerative disorders or skin disorders and for identifying cells
                                                                                                                                                                                                                                                                                                                                                                                                         EP908727-A1.
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                                                                                                                                   Sequence 720 BP; 173 A; 209 C; 215 G; 123 T; 0 U; 0 Other;
                                                                                                                                                                                                                    Claim 29;
                                                                                                                                                                                                                                                  diagnosing
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UNIV ST ANDREWS.
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ValValArgLysGluAspLeuArgProSerAlaProGlnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                    Page 16-17; 39pp; English.
                                                                                                                                                                                                                                                ein protein (persyn) and gene, useful in assays for screening, or monitoring cancer, neurodegenerative disorders or skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                             97GB-00019879
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Matches:
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GTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAG 369

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RESULT 11
ABS76519
        CC patient is afflicted with ovarian cancer. The method involves comparing CC patient is afflicted with ovarian cancer. The method involves comparing CC the expression level of a marker in a patient sample and the normal level CC of expression of the marker in a control non-ovarian cancer sample, where CC the marker is selected from 363 cancer markers described in the CC specification. The method of the invention is useful in diagnosing or CC characterising cancer, in detecting the presence of cancer as early as CC possible, and the recurrence of ovarian cancer. The method may also be of CC particular use with patients having an enhanced risk of developing CC ovarian cancer (e.g. patients having a familial history of ovarian CC cancer). The cancer markers may be used in the management and treatment CC of e.g. brain and central nerrous system disorders (e.g. bacterial and CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain CC inflammations (e.g. bacterial or viral meningitis or encephalitis), CC inflammations (e.g. bacterial or or viral meningitis or encephalitis),
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14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325149P.
testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determine whether ovarian cancer has metastasized or is likely to metastasize,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     central nervous system disorder; bacterial meningitis; viral mening: Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocep; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 411; 481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding human ovarian cancer marker OV60.
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                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to a new method for assessing whether
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer patient
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Morrisey MP, Olandt PJ, Sen A, Vieby PO,
א K, Schmandt RE, Zhao X, Glatt K;
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O, Mills
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Best Local Similarity:
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08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-033863P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selecting a composition for inhibiting ovarian cancer, assessing ovarian carcinogenic potential of a compound, or inhibiting ovar cancer or at risk of developing ovarian cancer. The present nucl sequence encodes one of the ovarian cancer markers described in
                                                                                                                                                                                                                                     Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2002;
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The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease is subject. The method comprises detecting in a target nucleic acid ob from the subject the presence or absence of an allelic variant of comore polymorphic regions of one or more genes selected from up (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (ine degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal

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08-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; neurodegenerative disease; urokinase plasminogen activator; gamma-symuclein; SNCG; insulin degrading enzyme; IDE; kinesin-like protein 1; KNSLI; lysosomal acid lipase; LIPA; tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease;
                                                                                                                                                                                      Determining a predisposition for or the occurrence of neurodegenerative disease, particularly Alzheimer's disease, comprises determining the presence of a polymorphism in the uPA, SNCG, IDE, XNSL1, LIPA or TNFRSFG
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07-SEP-2001 vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; Homo WO200164835-A2 sapiens. system disorders; arthritis; inflammation;

26-FEB-2001; 2001WO-US004927.

28-FEB-2000; 18-MAY-2000; 2000US-00515126. 2000US-00577409.

(HYSE-)

ĭ, Liu 'n Drmanac RT

P-PSDB; 2001-514838/56 AA013847

Isolated nucleic acids and polypeptides, useful, for preventing and treating e.g. leukemia, inflammation and immune disorders. diagnosing

Claim 1; SEQ ID NO 13838; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, innunomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and ç

This invention relates to a novel method of determining a predisposition for or the occurrence of neurodegenerative disease comprising detecting in a target nucleic acid obtained from the subject the presence of an

Claim 84;

SEQ ID NO 469; 205pp; English.

inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

ঠ ភភពXX RESULT 15 밁 US-09-017-715A-2\_COPY\_94\_107 (1-14) x AAI93778 (1-783) Percent Similarity: Best Local Similarity: Alignment Scores: Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antegonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds. New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases. 08-MAR-2000; 2000WO-US005881 WO200055173-A1. AAF21784; Sequence 783 BP; 187 A; 232 C; antifungal; antiparasitic and cardiant activity. Rosen CA, 12-MAR-1999; 21-SEP-2000 Homo sapiens. Human breast and ovarian cancer associated antigen gene SEQ ID 171. 27-MAR-2001 AAF21784 standard; DNA; 796 (HUMA-) HUMAN GENOME SCI INC Match: 2000-611515/58. )B; AAB58881. 1; Page 608; 1299pp; English. 1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln GTGGTGCGCAAGGACTTGAGGCCATCTGCCCCCCAACAG 434 Ruben SM (first entry) 99US-0124270P 0.0078 70.00 100.00% 100.00% ВP 237 G; 127 T; 0 U; 0 Other; Length:
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                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 381)

Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens full open reading frame cDNA clone RZPDo834B0231D for gene SNCG, synuclein, gamma (breast cancer-specific protein 1); complete cds, without stopcodon.
                                               Direct Submission
                                                            2 (bases 1 to 381)
Halleck, A., Ebert, L., Mkoundinya, M.,
Neubert, P., Kstrang, K., Schatten, R.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
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                                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                           280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
The codon is followed by the 3 att site: GACCCAGCTITCIT. .att
The clone is validated by the 3 att site: GACCCAGCTITCIT. .att
Compared to the reference sequence BC014098
we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
CR541788.1 GI:49456532 Full ORF shuttle clone, Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact RZPD (customer.service@rzpd.de) for further information Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH1304.01L
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heubnerweg 6, D-14059
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B0231D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                               complete cds, incl. stopcodon. CR541788
                                                                                                                                                                                    CR541788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available from RZPD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
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                                                                                                                                                                                                                                                                                      GTGGTGCGCAAGGACTTGAGGCCATCTGCCCCCCAACAG 321
                                                                                                                                                                                                                                                                                                                   ValValArgLysGluAspLeuArgProSerAlaProGlnGln 14
                                                                                                                            384 bp mRNA linear PRI 29-JUN-2004 sapiens full open reading frame cDNA clone RZPDo834F0930D for SNCG, synuclain, gamma (breast cancer-specific protein 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /proteIn_id="CAG46589.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="SNCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="SNCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Human Full ORF Clones Gateway(TM) -
/lab_host="DH5Alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                             Gateway(TM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pDONR201, Site_1: attP1; Site_2: attP2'
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Matches:
Conservative:
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Indels:
                             complete cds
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AUTHORS
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     Query Match:
                             Best Local Similarity:
                                                     Percent Similarity:
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                                                                                                                                                                                    ORIGIN
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                                                                                                          No ::
                                                                                                                                 Scores:
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1 (bases 1 to 384)

Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Meubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the codon: att. .AAAAAA GCA GGC TCC ACC (ATG).

The stopcodon is followed by the 3' att site: GACCCAGCTTCCTT.

The clone is validated by full sequence check.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact RZPD (customer.service@rzpd.de) for further information. Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH131021.01X
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RZPD; RZPDo834F0930D, ORFNO 3605
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
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Halleck, A., Eberr, L., Mkoundinya, M.,
Neubert, P., Kstrang, K., Schatten, R.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry vector (pDONR201)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +49 30 32639 100 Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.rzpd.de/products/orfclones/
Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomforschung GmbH,
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ne distribution: http://www.rzpd.de/products/orfclones/
                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                gene="SNCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
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/db_xref="taxon:9606"
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0.00395
70.00
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                                                                            Length:
Matches:
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                               Mismatches:
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                    ACCESSION
VERSION
KEYWORDS
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AR412236
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AUTHORS
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Best Local Similarity:
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Homo sapiens :
AF411524
                                                                                                             Unknown.
Unclassified
                                                                                                                                                                             Sequence 1 from patent US
AR412236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-AUG-2001) Department of Biochemistry, Institute Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dan San Tiao, Beijing 100005, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 488)
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Direct Submission
                                                                                                                                       Unknown.
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                                                                                 Moore, P.A.
                                                                                                                                                                                                                                                           ValValArgLysGluAspLeuArgProSerAlaProGlnGln.14
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                                                     ADA2 polypeptides
t: US 6639052-A 1 28-OCT-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="SNCG; breast cancer-specific
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                                                                                                                                                                  GI:40167022
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Matches:
Conservative:
Mismatches:
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Dong
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AX331171
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KEYWORDS
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DEFINITION
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BD022727
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Mammary cancer-specific gen
Patent: JP 2001509564-A 1 2
HUMAN GENOME SCIENCES INC
PN JP 2001509664-A/1
PD 24-JUL-2001
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AX331171
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Mammalia, Eutheria, Primates,
1 (Dases 1 to 550)
Ji,H. and Rosen,C.A.
                                                                                                                      Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Catarrhini;
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screening using signature

Endress, G.

Vertebrata;

Euteleostomi;

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27-AUG-2002

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Hominidae;

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Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K.,
Rosen,C. and Shi,Y.E.
Identification of a breast cancer-specific gene, BCSG1, by direct
differential cDNA sequencing
Cancer Res. 57 (4), 759-764 (1997)
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Rosen,C. and Shi,Y.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUN-1997) Ped. Res.,
Center, 270-05 76th Ave., New Hyde
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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03-FEB-1997 US 60/037080
HONGJUN JI,CRAIG A ROSEN
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Location/Qualifiers
1. .550
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue_type="breast cancer"
/note="cDNA highly abundant in a
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
codon_start=1
                             /note="breast cancer-specific protein note; note
                                                                                              /gene="BCSG1"
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Indels:
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Sequence 6816 from Pater
CQ720882
CQ720882.1 GI:42281739
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 720)
                                          Homo sapiens
                                                                                    Analytical matter based E36333 E36333.1 GI:13022626
                                                                                                                                                                                                              1 ValValArgLysGluAspLeuArgProSerAlaProGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 02068579-A 6816 06-SEP-2002; PE Corporation (NY) (US)
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                                                                        JP 1999239488-A/1.
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KENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
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Analytical matter based on synuclein and novel synuclein protein

L Patent: JP 199239488-A 1 07-SEP-1999;

THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD

OS Homo sapiens (human)

PN JP 1999239488-A/1

PD 07-SEP-1999

PY 199923948-A/1

PD 07-SEP-1999

PY 21-SEP-1998

PF 21-SEP-1996

PI ANDREW SMITH MAKKARION,VALDIMIA RUVOVICHI BUCHIMAN, PI ARUN

MILWARD DAVIS

PC C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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US-09-017-715A-2_COPY_94_107 (1-14) x AF017256 (1-720)
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Submitted (04-AUG-1997) School of Biomedical Sciences, Univ. of St.
Andrews, Bute Medical Buildings, St. Andrews, Fife KY16 9TS,
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1 (bases 1 to 720)

Ninkina, N.N., Alimova-Kost, M.V., Paterson, J.W., Delaney, L., Cohen, B.B., Imreh, S., Gnuchev, N.V., Davies, A.M. and Buchman, V.L. Organization, expression and polymorphism of the human persyn gene Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
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KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shaemen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Rouffard, G.G., Blakesley, R.M., Touchman, J.W., Green, E.D.,
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1 (bases 1 to 738)

Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.

Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
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Primer A: No primer sequence
Primer B: No primer sequence
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/mol_type="genomic DNA"
/db_Xref="taxon:9606"
/clome_lib="Human DNA (Sequenom)"
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Series: IRAL Plate: 28 Row: p Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4507112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur
Sequencing Center (NISC),
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Contact: MGC help desk
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On Aug 19, 2003 this sequence version replaced gi:15559464.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/trānslation="mdvfkkgfsIakegvvgavektkggvtbaaektkegvmyvgakt
kenvvgsvtsvaektkeqanavseavvssvntvatktveeaenIavtsgvvrkedlrp
sapqqegeaskekeevaeeaqsggd"
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/lab_host="DH10B-R"
                                                                                                  /protein_id="AAH14098.1"
/db_xref="GI:15559465"
/db_xref="LocusID:6623"
/db_xref="MIM:602998"
                                                                                                                                                                                                                                                                                                                                             gene="SNCG"
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/db_xref="LocusID:6623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="SNCG"
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/clone="MGC:20132 IMAGE:4546444"
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Scores:

70.00 0.00722

Conservative:

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Percent Similarity:
Best Local Similarity:
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AUTHORS
                           RESULT 15
AF037207
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AUTHORS
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 LOCUS
DEFINITION
                                                                      문
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Homo sapiens gamma-synuclein
AF044311
AF044311.1 GI:3347841
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Hum. Genet. 103 (1), 106-112 (1998)
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Lavedan, C., Leroy, E., Dehejia, A., Buchholtz, S.,

Nussbaum, R.L. and Polymeropoulos, M.H.
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sapiens persyn gene, complete
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                                                                                                                                                                                                                                                                                              /translation="mdvfkkgfsiakegvvgavektkqgvteaaektkegvmyvgakt
KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
SAPQQEGVASKEKEEVAEEAQSGGD"
                                                                                                                                                                                                                                                                                                                                      /product="gamma-synuclein"
/protein_id="AAC27738.1"
/db_xref="GI:3347842"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                        "map="10q23; between markers WI-5226 and AFM225YD12"
join(1. .173,988. .1029,1356. .1483,3953. .4024,4314
product="gamma-synuclein"
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SOURCE
                                          Query Match:
DB:
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Best Local Similarity:
           US-09-017-715A-2_COPY_94_107 (1-14)
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="member of symuclein family; similar to the Homo sapiens persyn protein encoded by sequence presented in GenBank Accession Number AF017256"
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Envvgsvtsvaektkeganavsbavvssvntvatktveeaeklavtsgvvrkedlrp
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/protein_id="AAC36586.1"
/db_xref="GI:3642903"
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-Q=/Cgn2 1/USPTO_spool_h/US09017715/runat_04052005_100744_25608/app_query.fasta_1.661
-DB=GenEmbl -QFMT=fastap -SUFPIX==rg -MINMATCH=0.1 -LCOPCL=0 -LCOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LCCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=US09017715_@CGN 1 1_3970_@runat 04052005_100744_25608 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1 (bases 1 to 381)

Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway (TW) system
                                                                 2 (bases 1 to 381).
Halleck,A., Ebert,L., Mkoundinya,M.,
Neubert,P., Kstrang,K., Schatten,R.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens full open reading frame cDNA clone RZPDoB34B0231D gene SNCG, synuclein, gamma (breast cancer-specific protein 1); complete cds, without stopcodon.
                 Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 He
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AF010126 Homo sapi
CQ720882 Sequence
E3633 Analytical
AX004527 Sequence
AF017256 Homo sapi
BV177827 sqrm97020
BC014098 Homo sapi
BC014098 Homo sapi
AC102691 Mus muscu
AC113712 Rattus no
AC137025 Rattus no
AC13312 Rattus no
AC13312 Rattus no
AC13319 Mus muscu
AC13319 Mus muscu
AC013434 Homo sapi
AL357503 Human DNA
AC1357503 Human DNA
AC135987 Human DNA
AC1359887 HUMB MUSCU
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AC149695
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AC016560 Homo sapi
AC073774 Mus muscu
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Drosophil
Zebrafish
                                                                                    ein,S.,
Mar,W.,
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RESULT 2
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The CDS has been inserted into pDONR201 via a BP Clonase(TM)

reaction. Additional sequence has been added in front of the start
codon: att. .AAAAAA GCA GGC TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att

The clone is validated by full sequence check.

Compared to the reference sequence BC014098

we did not find any amino acid exchanges.

Clone distribution: http://www.rzpd.de/products/orfolones/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact RZPD (customer.service@rzpd.de) for further information. Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH130940.DL This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heubnerweg 6, D-14059 Berlin,
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                       CR541788.1 GI:49456532 Full ORF shuttle clone,
                                                                        complete cds,
CR541788
                                                                                                                   Homo sapiens full ope
gene SNCG, synuclein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RZPD; RZPDo834B0231D, ORFNo 3631
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B0231D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
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Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                         CR541788
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                                                                                                                                                                                                                                                                      sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human Full ORF Clones Gateway(TM) -
/lab_host="DH5Alpha"
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                                                                                                 incl. stopcodon
                                                                                                                        open reading frame
ein, gamma (breast
                         Gateway (TM), complete cds.
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                                                                                                                                                                    384 bp
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Matches:
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frame cDNA clone RZPDo834F0930D for
reast cancer-specific protein 1);
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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This CDS has been cloned incl. stopcodon. The CDS has been inserted into pDONR201 via a reaction. Additional sequence has been added i codon: att. .AAAAAA GCA GGC TCC ACC (ATG). The stopcodon is followed by the 3' att site: The clone is validated by full sequence check.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact RZPD (customer.service@rzpd.de) for further information. Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FtH31021.01X
This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +49 30 32639 100 Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH.
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germany
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry vector (pDONR201)
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Cloning of human full open reading frames in Gateway(TM) system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
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one distribution: http://www.rzpd.de/products/orfclones/
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   'gene="SNCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
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AR412236
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                                                                                                                                                                        Sequence 1 from patent US AR412236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-AUG-2001) Department of Biochemistry, Institute Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dan San Tiao, Beijing 100005, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han, C., Zhang, B.,
Direct Submission
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Mammalia; Eutheria; Primates;
1 (bases 1 to 488)
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Homo sapiens synuclein gamma
AF411524
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                                                                                                         Unclassified.
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                                                      ADA2 polypeptides
t: US 6639052-A 1 28-OCT-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="SNCG; breast cancer-specific protein 1"
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Eukaryota; Metazoa; Chordata; C. Mammalia; Eutheria; Primates; C. 1 (bases 1 to 550)

Ji,H. and Rosen,C.A.

Mammary cancer-specific gene 1
Patent: JP 2001509664-A 1 24-JUJ
HUMAN GENOME SCIENCES INC
PN JP 2001509664-A/1
PD 24-JUL-2001
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: WO 0194629-A 1680 13-DEC-2001; Avalon Pharmaceuticals (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Strandedness: Double;
CC Topology: Both;
FH Key Location/Qualifiers
FT CDS 12 .392.
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PR 03-FEB-1997 US 60/037080
PI HONGJUN JI, CRAIG A ROSEN
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Ji,H., Liu,Y.E., Jia,T., Wang,M.,
Rosen,C. and Shi,Y.E.
                                                                                                                                                                                                                                                                                                                                                                              Identification of a breast cancer-specific gene, BCSG1, differential cDNA sequencing Cancer Res. 57 (4), 759-764 (1997) \mathcal{F}\mathcal{U} \mathcal{H}
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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codon_start=1
                 /note="breast cancer-specific protein D amyloid-like"
                                                 gene="BCSG1"
                                                                                                                                 /tissue_type="breast cancer"
/note="cDNA highly abundant in a breast
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 720)
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KENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
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/db_xref="taxon:9606"
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Analytical matter based on synuclein and novel synuclein protein the patent: JP 1999239488-A 1 07-SEP-1999;

THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS, NYUROBA LTD OS Homo sapiens (human)
PN JP 199923948-A/1
PD 07-SEP-1999
PP 21-SEP-1999
PR 19-SEP-1999 B 19-98306283
PR 19-SEP-1997 B 9719879.0
PI ANDREW SMITH MAKKARION, VALDIMIA RUVOVICHI BUCHIMAN, PI ARUN MILWARD DAVIS
PC C12N15/09,A01K67/027,C12Q1/68,G01N33/53,C12N15/00 CC
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1 (bases 1 to 720)

Ninkina, N.N., Alimova-Kost, M.V., Paterson, J.W., Delaney, L., Cohen, B.B., Inreh, S., Gnuchev, N.V., Davies, A.M. and Buchman, V.L. Organization, expression and polymorphism of the human persyn gene Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
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pattern of expression"
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mol_type="mRNA"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 738.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Matches:
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                               Score:
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            Percent Similarity:
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                                                                      Scores:
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Contact: nisc_mgc@nhgri.nih.gov

Akhter.N., Ayēle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg Marrians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAL Plate: 28 Row: p Column: 20
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the following selection criteria: matched \overline{m}RNA gi: 4507112. Location/Qualifiers
SAPQQEGEASKEKEEVAEEAQSGGD"
                             /trānslation="mdvfkkGfSIakEGVvGAVEKTKQGVTEAAEKTKEGVmYVGAKT
KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
                                                                                                   /protein_id="AAH14098.1"
/db_xref="GI:15559465"
/db_xref="LocusID:6623"
/db_xref="MIM:602998"
                                                                                                                                                                                                                                                                                                                                                  'gene="SNCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonyms: SR, BCSG1"
/db_xref="LocusID:6623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="SNCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Colon, adenocarcinoma"
/clone_Tib="NIH_MGC_15"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                product="synuclein,
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Length: Matches: Conservative:

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AC102691
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Direct Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (CE 3) (bases 1 to 17706)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stone, J., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo. A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Vo. A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., Lanccque, K., Liu, G., Marous, B., Heaford, A., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lanccque, K., Liu, G., MacLean, C., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyeen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peeterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riec, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zaimor, A., and Zodv, M., J., Young, G., J., Zaimor, A., and Zodv, M., J., Young, G.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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Indels:
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RESULT 15
AC111772
                                                                                               VERSION
KEYWORDS
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Best Local Similarity:
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                                                                                                                                            ACCESSION
                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                              32827 GAAGAAGCCCAGAGCGGTGGAGAC 32850
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 31, 2004 this sequence version replaced gi:22325140. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                    AC111772.4 GI:25007013
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                            Rattus norvegicus clone CH230-169C7, ***, 6 unordered pièces.
                                                                                                                                                                                                                                                                                                                         1 GluGluAlaGlnSerGlyGlyAsp 8
                                                                                                                                            AC111772
                                                                                                                                                                                                          AC111772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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96252
96352
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119943
131511
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Center clone name: 273_A_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP24-273A2"
/clone_lib="RPCI-24 Male Mouse
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     map="10"
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88976: gap of 100 bp
96251: contig of 7275 bp in length
96351: gap of 100 bp
119842: contig of 23491 bp in length
119942: gap of 100 bp
131510: contig of 11568 bp in length
131610: gap of 100 bp
145791: contig of 14181 bp in length
145891: gap of 100 bp
177006: contig of 31115 bp in length
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Matches:
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7, ***
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anylebechi, V., Aoyagi, A., Ayodeji, M., Bara, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benadawan, E., Baden, H., Balwalo, K., Blaix, J., Blankenburg, K., Blyth, P., Brown, M., Bernstead, M., Cater, K., Coavacos, I., Ceasas, H., Center, A., Chu, J., Clavel, M., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Cater, K., Coyle, M., Cree, A., D., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Devila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Devila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Devila, M., Davis, C., Poster, M., Garza, M
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23665002. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Allen, C., Allen, H., Alsbrooks, S., Amin, A., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                             and separated
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Score:

1 GluGluAlaGlnSerGlyGlyAsp

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US-09-017-715A-2_COPY_120_127 (1-8) x AC111772 (1-255619)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                              Query Match:
                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_d
NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: Phrap; version 0.990329
Consensus quality: 212404 bases at least Q40
Consensus quality: 215959 bases at least Q30
Consensus quality: 217955 bases at least Q30
Consensus quality: 217955 bases at least Q20
Estimated insert size: 218715; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: GOBO
Center clone name: CH230-169C7
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7935
18982
19082
62575
62675
65975
66075
254374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
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                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
19082. .20748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (6736. .7529)
                                                                                                                                                                                                                                                                                              23484
                                                                                                                                                                                                                                                                'note="wgs_contig"
                                                                                                                                                                                                                                                                                           /note="wgs_contig"
23484 .25134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CH230-169C7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7834: contig of 7834 bp in length
7834: gap of unknown length
18981: contig of 11047 bp in length
19081: gap of unknown length
62574: contig of 43493 bp in length
62674: gap of unknown length
65974: contig of 3300 bp in length
66974: gap of unknown length
254373: contig of 188299 bp in length
254373: contig of 186299 bp in length
254473: gap of unknown length
255619: contig of 1146 bp in length.
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                                                                              100.00%
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41.00
                                                                                                                                                                                                                                                                                                                                                                                                              sequence:BH336366'
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Matches:
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Db 223025 GAAGAAGCACAGAGTGGAGGGGAC 223048
Search completed: May 4, 2005, 11:54:02
Job time: 489.669 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2 1/USPTO gpool h/US09017715/runat 04052005_100744_25608/app_query.fasta_1.661
-Q=/Cgn2 1/USPTO gpool h/US09017715/runat 04052005_100744_25608/app_query.fasta_1.661
-DB=GenEmbl -QFMT=fastap -SUFFIX=Tge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=Ext -HEAPSIZE=50 -MINLEN==0 -MAXLEN=2000000000
-USER=US09017715 @CGN 1 13970 @runat 04052005_100744_25608 -NCPU-6 -TCPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NORM=EXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                         FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    Score
 010
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Ygapop 10.0 , y
Fgapop 6.0 , E
Delop 6.0 , I
 100.0
100.0
100.0
                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                             GenEmbl: *
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AR412236 Sequence
AX331171 Sequence
BD022727 Mammary c
AF010126 Homo sapi
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728889 Sequence	CQ728889	σ,	546	50.4	307.5	
BT007765 Synt	BT007765	12	423		33	
57058 Homo sap	57058	9	423		3	
62310 Sequence	AX662310	0	423		S	
41653 Homo e	CR541653	9	420		9	
7764 Rattus sp.	RAT14KDAP	10	549		308	
F044672 Mus mu	AF044672	10	513		310	
054200	BC054200	5	1233		311	
36116 Gallus		σ	1190	:	311.5	
53512 Gallus	Ħ	ហ	1182	ŗ	311.5	
3860 Serinus can	ä	S	1234	:	314.5	
73008 synuc]		10	695	51.6	315	
F179273	AF179273	10	1181	•••	316	
Mus		10	1124	۲	316	
046764		10	1047		316	
07758	00775	10	1018		316	
550006 Rattus	5	10	1017		. 316	
50005	Y55000	10	1017	۳		•
73007 s	73(	10	695	۳	316	
072217 Xenopus		v	1180	u.	388.5	
055119 Xenopus	AY055119	ഗ	1040	65.3	398.5	
54269		ű	1046	<u>ب</u>	399.5	
762140 Xenopus	<b>R76</b>	σ	1120	7.	412	
53513 G	ω,	տ	873		438.5	
. nor	RNSDSYNGE	10	732		470	
518351 Ratt	1835	10	488	в.	476	
C028508 Mus	BC028508	10	748	81.5	497	
F017255	25	10	727	Ľ	497	
004529 Sequ	AX004529	σ	727	Ľ	9	
6334 Analyt	E36334	თ	727	_	9	
219257 Bos tauru	AF219257	4.	677		52	
V177827 sqnm	BV177827	11	738	7		
7256	AF017256	9	720	7.	9	
AX004527 Sequence	AX004527	Φ	720	7.	9	
4	E36333	თ	720	97.5	9	
411524 Homo	AF411524	9	488	7.	9	
C014098 H	C014	9	758		0	
720882 Sequenc	Q720	σ	704		602	
41788 Homo sa	541	o	384		0	
CR541790 Homo sapi	CR541790	9	381	98.7	0	

## ALIGNMENTS

AR412236							
LOCUS	AR412236	v	550 bp D	DNA	linear	PAT	PAT 18-DEC-2003
DEFINITION	Sequence 1	Sequence 1 from patent US 6639052.	6639052.				
ACCESSION	AR412236						
VERSION	AR412236.1	AR412236.1 GI:40167022					
KEYWORDS	•						
SOURCE	Unknown.						
ORGANISM	Unknown.						
	Unclassified	<u>a.</u>					
REFERENCE	1 (bases 1 to 550)	to 550)					
AUTHORS	Moore, P.A.						
TITLE	Human ADA2	Human ADA2 polypeptides					
JOURNAL	Patent: US	Patent: US 6639052-A 1 28-OCT-2003;	OCT-2003;				
FEATURES	5	Location/Qualifiers	rs				
source	۲.	550					
	, 'o	organism="unknown"	ָּהָ מַיּ				
	/m	<pre>'mol_type="genomic DNA"</pre>	C DNA"				
ORIGIN							
Alignment Scores:	cores:						
Pred. No.:		7.25e-44	Length:		550		
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Percent Similarity	ilarity:	100.00%	Conservative:	ive:	0		
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Query Match:	•	100.00%	Indels:		0		
DB:		6	Gaps: .		0		

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Sequence 1680 from Patent W00194629.
AX331171
AX331171.1 GI:18121805
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                                                                                                                                                                                                                                                                        gene sets
Patent: W
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          AGGCCATCTGCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAAGAGAAGTGGCAGAG
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                                                                                                                                                                                                                                                 : WO 0194629-A 1680 13-DEC-2001;
Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                            gene determination and therapeutic
                                                                                                                                                                                                       /organism="Homo sapiens"
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BD022727
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TITLE
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Homo sapiens
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 550)
Ji,H. and Rosen,C.A.
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JP 2001509664-A/1.
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Mammary cancer-specific
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                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Patent: JP 2001509664-A 1 24-JUL-2001;
HUMAN GENOME SCIENCES INC
PN JP 2001509664-A/1
PD 24-JUL-2001
PD 24-JUL-2001
PD 24-JUL-2001
PF 03-FEB-1998 JP 1998515053
PF 03-FEB-1997 US 60/037080
PI HONGJUN JI, CRAIG A ROSEN
PC
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Strandedness: Double;
CC Topology: Both;
FH Key Location/Qualifiers
FT CDS 12..392.
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            LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal
                                                           MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
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                  Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUN-1997) Ped. Res.,
Center, 270-05 76th Ave., New Hyde
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 550)
Ji,H., Liu,Y.E., Jia,T.,
Rosen,C. and Shi,Y.E.
Direct Submission
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Ji,H., Liu,Y.E., Jia,T., Wang,M., Liu,J., Xiao,G., Joseph,B.K., Rosen,C. and Shi,Y.E.

Identification of a breast cancer-specific gene, BCSG1, by diredifferential cDNA sequencing

Cancer Res. 57 (4), 759-764 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCCCAGAGTGGGGGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (human)
                                                                                                                                                                                                  /gene="BCSG1"
/note="breast cancer-specific
AD amyloid-like"
                                                                             /codon start=1
/product=#ECSG1 protein"
/protein id=#ABB4109.1"
/db_xref="G1:2281474"
/db_xref="G1:2281474"
/translation="MDVFKKGFSIAKKGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
KENVVQSVTSVAEKTKEQANAVSKAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
SAPQQEGEASKEKEEVAEEAQSGGD"
                                                                                                                                                                                                                                                            /gene="BCSG1"
12. .395
                                                                                                                                                                                                                                                                                                         /tissue type="breast cancer"
/note="cDNA highly abundant in a
not in normal library"
                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
 7.25e-44
610.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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cancer-specific protein 1 (BCSG1) mRNA,
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Length:
Matches:
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NY 11040, USA
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 127
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                                                                                                                                                                                                                          synuclein-like;
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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CR541790
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VERSION
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                        TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens full open reading gene SNCG, synuclein, gamma (b) complete cds, without stopcodo
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
                                                                                                                   www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDO834B0231D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                    RZPD; RZPD0834B0231D, ORFN0 3631
                                                                                                                                                                                                        Submitted (28-JUN-2004)
                                                                                                                                                                                                                                     Halleck,A., Ebert,L., Mkoundinya,M., Neubert,P., Kstrang,K., Schatten,R., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
                                                                                                                                                                                                                                                                                                                                          Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Neubert,P., Kstrang,K., Schatten,R., Shen,B., H. Korn,B., Zuo,D., Hu,Y. and LaBaer,J. Cloning of human full open reading frames in Gal
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR541790
CR541790.1 GI:49456536
                                                                www.rzpd.de/cgi-bin/products/showLib.pl
www.rzpd.de/products/orfclones/
                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                          entry vector (pDONR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full ORF shuttle clone,
                                                    Contact: Inge Arlart
                                                                                                                                                                                    Genomforschung GmbH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluAlaGlnSerGlyGlyAsp 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys
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                                                                                                                                                                                                                                                                                         (bases 1 to 381).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 bp mRNA linear PRI 29-JUN-2004 in reading frame cDNA clone RZPDo834B0231D for gamma (breast cancer-specific protein 1); stopcodon.
                                                                                                                                                                                      RZPD Deutsches Ressourcenzentrum fuer Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gateway (TM),
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                                                                                                                                                                                                                                                         Schick, M.,
Shen, B., He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete
                                                                                   .cgi/response?libNo=834
                                                                                                                                                                                                                                                                                                                                             Gateway (TM) system
                                                                                                                                                                                                                                                          Henze,
                                                                                                                                                                                                                                                                                                                                                                              Henze, S., Mar, W.,
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                                                                                                                                                                                                                                                         Bisenstein,S.,
enze,S., Mar,W.,
                                                                                                                                                                                                                                                                                                                                                                                                  Eisenstein, S.,
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US-09-017-715A-2 (1-127) x CR541790 (1-381)
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                       301
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                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The CDS has been inserted into pDONR201 via a BP Clonase(Two reaction. Additional sequence has been added in front of the codon: att. .AAAAA GCA GGC TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTTC The clone is validated by full sequence check. Compared to the reference sequence BC014098 we did not find any amino acid exchanges. Clone distribution: http://www.rzpd.de/products/orfclones/.location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact RZPD (customer.service@rzpd.de) for further information. Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH130940.0LL This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.rzpd.de
                                                                                                                                                                                                                                                                                                                               GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
                                               ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                                                                                                                                        ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           has been cloned without stopcodon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mdvfkkGfsIakEgvvGavekTkQGvTeaaekTkEgvmyvGakT
KENvvQSvTSvaEkTkEQANAvSEAvvSSvNTvaTkTvEeaENIAvTSGvvRkEdLrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/protein_id="CAG46589.1"
/db_xref="GI:49456537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector:
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/clone_lib="Human Full ORF Clones Gateway(TM) -
/lab_host="DH5Alpha"
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/db_xref="taxon:9606"
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602.00
100.00%
98.43%
98.69%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Direct Submission .

Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 384)

Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR541788 384 bp mRNA linear PRI 29-JUN-200-
Homo sapiens full open reading frame cDNA clone RZPDo834F0930D for
gene SNCG, symulein, gamma (breast cancer-specific protein 1);
                                                                                                                                                                                                                                                                                                                                                              This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a reaction. Additional sequence has been added i codon: att. AAAAAA GCA GCC TCC ACC (ATG).
The stopcodon is followed by the 3' att site:
The clone is validated by full sequence check.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                   we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (www.hip.harvard.edu): FLH131021.01X
This CDS clone is part of a collection of human
jointly established and verified by the Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH.
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.rzpd.de/products/orfclones/
Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834F0930D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RZPD; RZPD0834F0930D, ORFNO 3605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete cds, incl. stopcodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
                                                                                                                                                                                                                                                                                                                                                Compared to the reference sequence BC014098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteomics (HIP) and RZPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available from RZPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGCCCAGAGTGGGGGAGAC
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gene="SNCG"
                                          gene="SNCG"
                                                                                                                  /lab_host="DH5Alpha"
                                                                                                                              /clone="RZPDo834F0930D"
/clone_lib="Human Full ORF Clones Gateway(TM) -
                                                                                                                                                                                                          /mol_
                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                          note="Vector:
                                                                                                                                                                                     db_xref="taxon:9606"
                                                                     . 384
                                                                                                                                                                                                      type="mRNA"
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                                                                                                                                                                                                                                                                7 CQ720882 7 Sequence 6816 from Patent CQ720882 CQ720882.1 GI:42281739
                                                                                                                                     thereof
                                                                                                                                                humanexons or transcripts, for detecting
                                                                                                                                                          Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of
                                                                                                              Patent: WO 02068579-A 6816 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                         sapiens (human)
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/proteIn_id='CAG46587.1"
/broteIn_id='CAG46587.1"
/db_xref="GI:49456533"
/translation="MDVFKKGFSIAKEGVVGAVEKTKQGVTEAAEKTKEGVMYVGAKT
KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIAVTSGVVRKEDLRP
SAPQQEGEASKEKEEVAEEAQSGGD"
                                                                                                Location/Qualifiers
                                                /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                         organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                          Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Millahy, S. J., Bonsathe, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S. A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 758)
Strausberg, R.
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Strausberg,R.L., Fe
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   71
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@ahgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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On Aug 19, 2003 this sequence version repla
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                    MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20
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/db_xref="LocusID:6623"
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/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                   /db_xref="LocusID:6623"
/db_xref="MIM:602998"
                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAH14098.1"
/db_xref="GI:15559465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="SNCG"
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 21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal
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US-09-017-715A-2 (1-127) x AF411524 (1-488)
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Location/Qualifiers
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Submitted (19-AUG-2001) Department of Biochemistry, Institut
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 720)

Andrew S.M., Valdimia,R.B. and Arun,M.D.

Analytical matter based on synuclein and novel synuclein protein Patent: JP 199239488-A 1 07-SEP-1999;

THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS,NYUROBA LTD OS Homo sapiens (human)

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Location/Qualifiers
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19-SEP-1997 GB 9719879.0
ANDREM SMITH MAKKARION, VALDIMIA RUVOVICHI BUCHIMAN,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 720)

Ninkina,N.N., Alimova-Kost,M.V., Paterson,J.W., Delaney,L., Cohen,B.B., Imreb,S., Gnuchev,N.V., Davies,A.M. and Buchman,V.L. Organization, expression and polymorphism of the human persyn gene Hum. Mol. Genet. 7 (9), 1417-1424 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF017256
Homo sapiens persyn mRNA,
AF017256
AF017256.1 GI:3642774
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-AUG-1997) School of Andrews, Bute Medical Buildings, 9
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Buchman, V.L.
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          MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
                                                                                                                                                               433. .720
684. .689
706
                                                                                                                                                                                             /protein_id="AAC36550.1"
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SAPQQEGVASKEKEEVAEEAQSGGD"
                                                                                                                                                                                                                                                                           /note="member of the synuclein family with pattern of expression"
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                  Scores:
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Primer B: No primer sequence
STS size: 738.
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3595 John Hopkins Court, San Diego,
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Andreas Braun Pharmaceuticals division
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 738)
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                                                                                                                                                                                                                                                                                                                 Email: abraun@sequenom.com
                                                                                                                                                                                                                                                                                                                                                Tel: 1858202901
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Bos taurus :
AF219257
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Submitted (27-DEC-1999) Ophthalmology, Washington University School of Medicine in St. Louis, 660 South Euclid, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 677)
Surguchov, A., Surgucheva, I., Solessio, B. and Baehr, W.
Synoretin.—A new protein belonging to the synuclein family
Mol. Cell. Neurosci. 13 (2), 95-103 (1999)
                                                                                                                                                                                                                                                                                                       USA
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Mammalia; Eutheria;
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                                                                                                                                                                          /note="member of gamma-subfamily of synuclein;
persyn; expressed in retina and brain"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                       organism="Bos taurus
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synoretin mRNA, complete
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   2.67e-36
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xref="taxon:9913"
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Length:
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ORGANISM
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Analytical matter based of
E36334.1 GI:13022627
E36334.1 GI:13022627
JP 1999239488-A/2.
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                                                                                                                                                                                                                   Analytical matter based on synuclein and novel synuclein |
Patent: JP 199239488-A 2 07-SEP-1999;
THE UNIVERSITY COURT OF THE UNIVERSITY OF ST ANDREWS, NYURO
OS Mus musculus (mouse)
PN JP 199239488-A/2
PD 07-SEP-1999
PP 21-SEP-1999
PF 21-SEP-1999
PF 21-SEP-1997
PF 21-SEP-1997
PF 19-SEP-1997
PF ANDREW SMITH MAKKARION, VALDIMIA RUVOVICHI BUCHIMAN, I
MILMARD DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 727)
Andrew,S.M., Valdimia,R.B. and Arun,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal
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Location/Qualifiers
                                                                                                                                                      (69)..(440).
Location/Qualifiers
                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
4.93e-34
497.00
89.76%
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727
108
6
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linear

PAT 18-JUN-2001

300

240

360

synuclein

protein.

Euteleostomi;
; Murinae; Mus

protein

ARUN

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-MODEL-Frame+_p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool h/US09017715/runat_04052005_100747_25719/app_query.fasta_1.661
-Q=/cgn2 1/USPTO_spool h/US09017715/runat_04052005_100747_25719/app_query.fasta_1.661
-DB=PublIshed_Applications_NA -QFMT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATTRIX=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09017715 @CGN 1 1 684 @runat 40452005 100747_25719
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDEXT=0.5
-FGAPDOP=6 -FGAPEXT=7 -YGAPDOP=10 -YGAPDEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_FUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_FUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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m2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 27013, A	equence 1316	e /5512	equence 129	equence 14517	equence 1265	equence 4491	equence 119	equence 10074,	equence 6521,	equence 667	equence 6547,	equence 3503,	e 27423,	equence 65435,	Sequence 1.	98. Apr	equence 1, Appr	) (C	equence 48, App	equence 1099	equence 12322	equence 12322	e 1232	equence 12322	equence 15323,	equence 43087,	equence 1775	equence 8217,	equence 90466	equence 33	Sequence 171.	CC 40),	200,	equence 297,	equence 1680,	equence 1,	quence 613, Ap	equence 2705,	ce 172,	uence 172, Ap	Sequence 5, Appli	ň

## ALIGNMENTS

RESULT 1 US-10-826-157-5

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Sequence 5, Application US/10826157

Publication No. US20050064548A1

GENERAL INFORMATION:
APPLICANT: Lindquist, Susan L.
APPLICANT: Outeiro, Tiago
TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
FILE REFERENCE: 17481-003001
CURRENT APPLICATION NUMBER: US/10/826,157
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/472,317
PRIOR APPLICATION NUMBER: US 60/463,284
PRIOR FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 384
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US-10-826-157-5

TYPE: DNA ORGANISM: Homo

sapiens

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GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA103PIC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SET IN MCS. 846
                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-102-806-172
; Sequence 172, App
; Publication No. 1
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 172
LENGTH: 478
TYPE: DNA
SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                     SOFTWARE: PatentIn Ver.
                                        NUMBER OF SEQ ID NOS: 846
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o. US20020039764A1
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Matches:
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
INUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2705
LENGTH: 479
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Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2705, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                   APPLICANT: Weaver, Zoe
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NAME/KEY: misc_feature
LOCATION: (1)...(479)
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Matches:
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US-10-453-478-1
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US-09-954-531-613
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PRIOR PILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                    APPLICATION NUMBER: US/08/705,771

PILING DATE: August 30, 1996

ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/453,478
FILING DATE: 04-Jun-2003
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 II
                      TOPOLOGY: lin
MOLECULE TYPE: DNA
                                                                                                                             SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                         LENGTH: 550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSELAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
US-10-097-340-297; Sequence 297, Application US/10097340
                                                                                                                                                       US-09-017-715A-2_COPY_120_127 (1-8) x US-10-843-641A-1680 (1-550)
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-10-843-641A-1680
                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1680
LENGTH: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1680, Application US/10843641A
Publication No. US20050064454A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR FILING DATE: 2001-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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APPLICATION NUMBER: US/09/962,832
FILING DATE: 2001-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/967,768
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Indels:
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Indels:
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Conservative:
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Publication

No. US20030087250A1

APPLICANT: John MONAHAN APPLICANT: Manjula GANI

Manjula GANNAVARAPU

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APPLICANT: AGENCY
APPLICANT: AGENCY
APPLICANT: AGENCY
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/376,026
PRIOR APPLICATION NUMBER: 60/377,026
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/310,732
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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SEQ ID NO 297
LENGTH: 720
TYPE: DNA
                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
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PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
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  APPLICANT
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No.:
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Rachel E. MEYERS
Michael MORRISEY
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Xumei ZHAO
Karen GLATT
                     Bertram, Lars
Saunders, Aleister J.
Mullin, Kristina M.
                                                                                       Wang, Xin
Tanzi, Rudolph E.
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Robert C. BAST, Jr.
Sampson, Andrew Johnson
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o. US20030224380A1
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APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister Johnson
APPLICANT: Saunders, Aleister Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND OTHER ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
FILE REFERENCE: 37481-3308B
CURRENT APPLICATION NUMBER: US/10/600,009
CURRENT FILLING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
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DB:
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Best Local Similarity:
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APPLICANT: Becker, I
APPLICANT: Velicel
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APPLICANT:
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TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/282,174
CURRENT FILING DATE: 2002-10-25
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NAME/KBY: allele
LOCATION: 30,57,85,243,250,377,512,531,555,561,672
OTHER INFORMATION: N is any
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APPLICATION NUMBER: US 60/338,363
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Wang, Xin
Tanzi, Rudolph E.
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Matches:
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Indels:
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RESULT 12
US-10-102-806-171
; Sequence 171, Application US/10102806
; Publication No. US20030054421A1
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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US-09-925-298-171
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Best Local Similarity:
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; LOCATION: 30,57,85,243,250,377,512,531,555,561,672
; OTHER INFORMATION: N is any
US-10-600-009-469
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SEQ ID NO 171
LENGTH: 796
TYPE: DNA
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Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
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LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/282,174
PRIOR APPLICATION NUMBER: US 10/282,174
PRIOR PILING DATE: 2002-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                   466 GAGGAGGCCCAGAGTGGGGGAGAC 489
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Coddman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITITLE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 33286
LENGTH: 1125
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                                                    US-09-017-715A-2_COPY_120_127 (1-8) x US-10-369-493-33286 (1-1125)
                                                                                                                                         Percent Similarity:
Best Local Similarity:
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DB:
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-806-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-369-493-33286/c
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 846
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                                                                                                                                                                                                                                                                                       ORGANISM: Desulfitobacterium hafniense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 GAGGAGGCCCAGAGTGGGGGAGAC 489
1 GluGluAlaGlnSerGlyGlyAsp
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Matches:
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Mismatches:
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RESULT 14

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609 GAAGAAGCCCAGGCCGGTGGCGAC 586

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Percent Similarity:
Best Local Similarity:
Query Match:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-437-963-8217
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APPLICANT: LIA PING
APPLICANT: LIA PING
APPLICANT: LIA PING
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(52221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 8217
LENGTH: 2185
TYPE: DNA
ORGANISM: Oryza Sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_14742C.1
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 90466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90466, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8217, Application US/10437963 Publication No. US20040123343A1
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LOCATION: (1)..(442)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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ORGANISM: Zea mays
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Indels:
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-Q=/Cgn2 1/USPTO spool h/USO9017715/runat 04052005 100745 25632/app query.fasta_1.661
-DB=16sued Patence NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=DLOSum62 -TRANS-buman40.cdi
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Maximum Match
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seq length:
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Delop 6.0,
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Match
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-949-016-152

US-09-949-016-17292

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           Sequence 1, Appli
Sequence 1, Appli
Sequence 1915, Ap
Sequence 442, App
Sequence 5550, Ap
Sequence 1, Appli
Sequence 12, Appl
Sequence 17292, A
Sequence 11824, A
Sequence 11824, A
Sequence 11824, A
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US-08-705-771-1
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                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
                                APPLICATION NUMBER: US/08/705
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
             TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                        ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           STATE: NEW JI
COUNTRY: USA
                                                                                                                                                                                                                                                    STREET: 6 BECKER FARM CITY: ROSELAND
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
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US-09-621-976-18782
US-09-621-976-18788
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US-09-949-016-26509
US-09-949-016-164928
US-09-949-016-202311
US-09-338-33-156
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US-09-215-681-156
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US-09-216-003A-156
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US-09-949-016-49739
US-09-328-111-367
US-09-830-111E-1
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US-09-270-767-26942
US-09-270-767-25543
                                                           325800-346 (PF196)
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16284, A 187123, A 187123, A 187127, A 18728, A 18728, A 18728, A 13044, A 13044, A 13044, A 13044, A 13046, A 1305, A 18762, A 1

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Percent Similarity:
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Percent Similarity:
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                                                           Pred. No.:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEPAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTMARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,540
FILING DATE: 14-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                 MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
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                                                                                                                                                                                   LENGTH: 550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
                                                                                                                                                                                                                                                                                                                                                              NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ROSELAND
STATE: NEW JERSEY
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                 Matches:
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; ORGANISM: Human
US-09-949-016-1915
US-09-949-016-442
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                                                                                                                                                                  Sequence 442, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1915
LENGTH: 702
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                    SOFTWARE: Fa
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
                                                                                                           PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-10-20
                    LENGTH: 720
TYPE: DNA
ORGANISM: Human
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APPLICANT: Storm, Daniel K.
APPLICANT: Hacker, Beth
APPLICANT: Tomlinson, James E.
APPLICANT: Tomlinson, James E.
APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
ITILE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
ITILE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5029-01-US
CURRENT APPLICATION NUMBER: US/09/473,717
CURRENT APPLICATION NUMBER: D99-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR APPLICATION NUMBER: D99-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
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Best Local Similarity:
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US-09-949-016-5550
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US-09-949-016-5550/c
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Best Local Similarity:
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SEQ ID NO 5550
LENGTH: 1902
TYPE: DNA
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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Patent No. 6372475
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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US-09-398-193-98/c
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Best Local Similarity:
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Query Match:
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GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                            Sequence 98, Application US/09398193 Patent No. 6197581
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SEQ ID NO 152
LENGTH: 4985
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SEQ ID NO 1
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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NUMBER OF SEQ ID NOS: 207012
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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ÖRGANISM: human type IX adenylyl cyclase
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NAME/KEY: CDS
LOCATION: (17)..(3898)
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/09/1755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 270012
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Best Local Similarity:
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Pred. No.:
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; NAME/KEY: CDS
; LOCATION: (539)..(4600)
US-09-398-193-98
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                                                                                                         US-09-949-016-11824/c
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Best Local Similarity:
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Sequence 11824, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 5515
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Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FRECSEQ for Windows Version 4.0
SEQ ID NO 13193
LENGTH: 126200
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Best Local Similarity:
Query Match:
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                                        Percent Similarity:
Best Local Similarity:
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; OTHER INFORMATION: n = A
US-09-949-016-13193
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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LENGTH: 126200
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NAME/KEY: misc_feature
10...(126200)
                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                     FEATURE:
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87.50%
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                   Conservative: Mismatches: Indels:
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Matches:
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US-09-017-715A-2\_COPY\_120\_127 (1-8) x US-09-949-016-13193 (1-126200)

1 GluGluAlaGlnSerGlyGlyAsp 8

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Best Local Similarity:
                                               Alignment Scores: Pred. No.:
                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-17207
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US-09-949-016-11894
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Patent No. 6812339
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LENGTH: 154605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Matches:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Best Local Similarity:
Query Match:
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; ORGANISM: Human
US-09-949-016-49739
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Best Local Similarity:
                                                     APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Catrino, Theodore J.
APPLICANT: Catrino, Theodore J.
APPLICANT: Pord, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GE
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: Steinmann, Ka
APPLICANT: Astle, Jon H.
EARLIER APPLICATION NUMBER: US 60/088,801
                   CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 601
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OF DETECTION AND USES THEREOF
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Minimum
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-Q-(cgn2 1)(USPTO spool h)(US09017715/runat 04052005 100747 25719/app query.fasta_1.661
-DB-Published_Applications_NA -QFMT=fastap SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS_bits -STAXT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MXX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09017715 @CGN 1 684 @runat 04052005 100747 25719
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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DB seq length: 2000000000
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Ygapop 6.0 , Fgapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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                                                                                                  /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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                    _6/ptodata/1/pubpna/US10 NEW PUB.seq:*
_6/ptodata/1/pubpna/US11 NEW PUB.seq:*
_6/ptodata/1/pubpna/US60 NEW PUB.seq:*
  _6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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748.404 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	610	100.0	550	إو	US-09-954-531-613	Sequence 613, App
2	610	80.	550		S-10-453-478-1	ce 1, App
. ω	610	100.0	· UI	19	S-10-843-641A-	Sequence 1680
л.44.п	602		796 796		-10-103-806-	171, App
ס נ	595	7 9	384	19	S-10-826-157-5	Sequence 5, Appli
7	595	97.5	2		-10-097-	e 297, Ap
8	592	.7	720	17	S-10-282-174-4	e 469,
. 9	592	7.	N	19	-10-600-009-46	e 469,
	538	88.2	7	10	-09-918-995-27	e 270
	468.5	٠,	₿	14	-10-267-E	1, Ag
12	w	w		18	-10-204-337A	(D)
13	316	1.	1018	17	-10-152-319A-	e 171
14 .	. 316	51.8		19	706-2	N
15	12.	۲.		18	-10-737-	2
16	07.				-10-077-	,
17	٠	.0	N	18	-10-204-337A	·ω
. 12	27	٠.	423	. L	-10-826-157-	
	307.5	<b>&gt;</b>	1105		IIS-10-223-978-10	sequence 1, Appli
21	07	0 :	1466	15	-10-101-51	36
	07.		54	18	8-10-721-693-14	14,
23	97.	0	1543	18	-10-	e 14,
24	304.5	.9	755	17	S-10-112-944-11	Sequence 11,
25	304	9	441	v	-09-960-352-126	equence 12619
26	30	9.	453	و	60-352-502	5029,
27	•	. 9	1096	10	921-406C-	, ,
200	33	9.	1096	18	-10	2 23
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30	302		• 0	19	-10-826-157-3	0 14
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39	201.5		ဌ	17	-10-282-174-4	483,
	•	$\omega \omega \iota$	2	19	-10-600-009-48	483, Ap
			132		-10-029-386-2579	e 25796
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c 41 c 42	199 199	~~~~	502	16	-10-029-386-120	3
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4444			5666 5666	16 17 19	-10-029-386-1209 -10-282-174-73 -10-600-009-73	Sequence /3, Appl Sequence 73, Appl

#### ALIGNMENTS

US-09-954-531-613

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Sequence 613, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
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RESULT 2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10453478 Publication No. US20030208043A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 550
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/453,478
FILING DATE: 04-Jun-2003
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                             APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
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                                                                                                                                                                                                                                                                                                                                                                                                             GluAlaGlnSerGlyGlyAsp 127
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                                                                                                                               STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
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CECCHI, STEWART & OLSTEIN
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                                                                                                                                                                                   ; Sequence 1680, Application US/10843641A; Publication No. US20050064454A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          RESULT 3
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                                                                                                                                                                                                                                                     US-10-843-641A-1680
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
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REFERENCE/DOCKET NUMBER: 3588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEPAX: 973-994-174
ORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches:
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-925-298-171
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; ORGANISM: Homo sapiens
US-10-843-641A-1680
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Sequence 171, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
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LENGTH: 550
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SOFTWARE: PatentIn version 3.0
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OR APPLICATION NUMBER: US/09/962,436

OR FILING DATE: 2001-09-25

OR APPLICATION NUMBER: US/09/962,832

OR FILING DATE: 2001-09-25

OR FILING DATE: 2001-09-25

OR APPLICATION NUMBER: US/09/964,824

OR APPLICATION NUMBER: US/09/967,768

OR APPLICATION NUMBER: US/09/967,768

OR FILING DATE: 2001-09-28

OR FILING DATE: 2001-09-28
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FILING DATE: 2001-10-02
APPLICATION NUMBER: US/09/969,347
FILING DATE: 2001-10-02
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APPLICATION NUMBER: US/09/954,456
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; LENGTH: 796
; TYPE: DNA
; ORGANISM: Homo s
US-09-925-298-171
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PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 171
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US-10-102-806-171
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Query Match:
                                                                             FILE REFERENCE: PA103PIC1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
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                                                 SOFTWARE: Patentin Ver.
SEQ ID NO 171
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TITLE OF INVENTION: Nucleic Acids, Proteins
LENGTH: 796
TYPE: DNA
ORGANISM: Homo sapiens
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o. US20030054421A1
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APPLICANT: Lindquist, Susan L.

APPLICANT: OuteAiro, Tiago

TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
TITLE OF INVENTION: PROCESSED PROTEINS AND USES THEREFOR
FILE REFERENCE: 17481-003001
CURRENT APPLICATION NUMBER: US/10/826,157
CURRENT FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/472,317
PRIOR APPLICATION NUMBER: US 60/472,317
PRIOR APPLICATION NUMBER: US 60/463,284
PRIOR FILING DATE: 2003-05-20
PRIOR FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5
LENGTH: 384
TYPE: DNA
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     US-09-017-715A-2 (1-127) x US-10-826-157-5 (1-384)
                                                                          Percent Similarity:
Best Local Similarity:
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US-10-826-157-5
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Best Local Similarity:
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Publication No. US20050064548A1
GENERAL INFORMATION:
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                   . No.:
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Matches:
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CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR PELICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR PELICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-09-16
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
NUMBER: 67 SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 720
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APPLICANT: Manjila GANEA
APPLICANT: Schastian GANEA
APPLICANT: Schubhangi KAM
APPLICANT: Shubhangi KAM
APPLICANT: Steve G. KOVA:
APPLICANT: Rachel E. MEZI:
APPLICANT: Michael MORRIO
APPLICANT: Peter OLANDT
APPLICANT: ANI SEN
APPLICANT: Gordon B. MILI
APPLICANT: Robert C. BASS
APPLICANT: Robert C. BASS
APPLICANT: Karen LU
APPLICANT: Xumei ZHAO
APPLICANT: Xumei ZHAO
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLÄTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 297, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For TITLE OF INVENTION: Assessment, Prevention, and Therapy of FILE REFERENCE: MRI-030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Rachel E. MEYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGCCCAGAGTGGGGGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosemarie SCHMANDT
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The Identification, Ovarian Cancer

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APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Kathryn J.
APPLICANT: Wang, Xin
APPLICANT: Wang, Xin
APPLICANT: Bartram, Lars
APPLICANT: Bertram, Lars
APPLICANT: Mullin, Krietina M.
APPLICANT: Mullin, Krietina M.
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Krietina M.
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND TITLE OF INVENTION NUMBER: US/10/282,174
CURRENT APPLICATION NUMBER: US/10/282,174
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR APPLICATION NUMBER: US 60/338,363
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US-10-282-174-469
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; ORGANISM: Homo
US-10-097-340-297
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Query Match:
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5. US20030224380A1
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Sequence 469, Application US/1060000
Publication No. US20050009031A1
GENERAL INFORMATION:
APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Ellick, Kathryn J.
APPLICANT: Wang, Xin
APPLICANT: Wang, Xin
APPLICANT: Bertram, Lars
APPLICANT: Seunders, Aleister J.
APPLICANT: Sampson, Andrew Johnsor
APPLICANT: Blacker, Deborah Lynne
APPLICANT: Blacker, Deborah Lynne
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, NAME/KEY: allele
, LOCATION: 30,57,85,243,250,377,512,531,555,561,672
; OTHER INFORMATION: N is any
US-10-282-174-469
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Best Local Similarity:
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DB:
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 469
LENGTH: 720
                                                 APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE A
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
FILE REFERENCE: 37481-3308B
CURRENT APPLICATION NUMBER: US/10/600,009
CURRENT FILING DATE: 2003-06-18
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                                                                                                                                    Tanzi, Rudolph E.
Bertram, Lars
Saunders, Aleister J.
Mullin, Kristina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu
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                                                                                                                                                                                                                                                                                               Application US/10600009 o. US20050009031A1
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APPLICATION NUMBER: US 60/339,525

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RESULT 10
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DB:
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR PRILING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-09
PRIOR PELLING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2002-03-28
PRIOR PELLING DATE: 2002-03-28
PRIOR PELLING DATE: 2002-10-25
PRIOR PELLING DATE: 2002-10-25
PRIOR PELLING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 564
Sequence 2705, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 30,57,85,243,250,377,512,531,555,561,672
OTHER INFORMATION: N is any
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                                                                                                                                                                         GAGGCCCAGAGTGGGGGAGAC
                                                                                                                                                                                                                                        ACCGTGGAGGAGGCGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG
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US-10-267-849-1

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ILENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE;
; NAME/KEY: misc feature
; LOCATION: (1)...(479)
; OTHER IMFORMATION: n = A
US-09-918-995-2705
                            Sequence 1, Application US/10267849
PUDDICATION NO. US2030087824A1
GENERAL INFORMATION:
APPLICANT: Ji, Hongjun
APPLICANT: WORST Cancer Specific General Control of Title OF INVENTION: Breast Cancer Specific General Custom Application NUMBER: US/10/267,849
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US/08/673,284
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1995-06-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 786
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Best Local Similarity:
Query Match:
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US-10-267-849-1
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2705
TYPE: DNA
ORGANISM: Homo sapiens
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96.55%
88.20%
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Matches:
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; LENGTH: 210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-337A-5
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US-10-204-337A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10204337A Publication No. US20040128706A1 GENERAL INFORMATION:
APPLICANT: Maslish, Eliezer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method for screening for Anti-Amyloidogenic Properties and Method TITLE OF INVENTION: Treatment of Neurodegenerative Disease FILE REFERENCE: 6627-PC9014 CURRENT APPLICATION NUMBER: US/10/204,337A CURRENT FILING DATE: 2002-08-16 PRIOR APPLICATION NUMBER: B. 160/183,571 PRIOR APPLICATION NUMBER: WS 60/183,571 PRIOR PILING DATE: 2000-02-18 PRIOR FILING DATE: 2000-02-18 PRIOR FILING DATE: 2000-03-17 PRIOR PILING DATE: 2001-03-17 NUMBER: PCT/US00/07216 PRIOR FILING DATE: 2001-03-17 NUMBER: PCT/US00/07216 PRIOR FILING DATE: 2001-03-17 NUMBER: PCT/US00/07216 PRIOR FILING DATE: 2001-03-17 NUMBER: PCT/US00/07216 PRIOR PRIOR
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97.14%
53.77%
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86.15%
85.38%
76.80%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR APPLICATION NUMBER: US 60/303,808
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                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                              US-09-017-715A-2 (1-127)
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NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1710
LENGTH: 1018
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APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                   FEATURE:
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GluGlnAlaAsnAlaValSerLysAlaVal
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51.80%
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Matches:
Conservative:
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Indels:
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Query Match:
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Sequence 260, Application US/10486706
Publication No. US20050071088A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                   US-10-486-706-260
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENE EXPRESSION PROFILE BIOMARKERS AND THERAPEUTIC TARGETS
TITLE OF INVENTION: BRAIN AGING AND AGE-RELATED COGNITIVE IMPAIRMENT
FILE REPERENCE: 50229-426
CURRENT APPLICATION NUMBER: US/10/486,706
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: PCT/US02/25607
PRIOR APPLICATION UNMBER: US 60/311,343
PRIOR APPLICATION UNMBER: US 60/311,343
PRIOR APPLICATION UNMBER: US 60/311,343
PRIOR APPLICATION NUMBER: US 60/311,343
PRIOR PRILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 461
SOFTWARE: Patentin version 3.2
SEQ ID NO 260
LENGTH: 1018
TYPE: DNA
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                                GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
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               GGTTCCAAAACTAAGGAGGGAGTCGTTCATGGAGTGACAACAGTGGCTGAGAAGACCAAA
                                                                                                                                     BLALOCK, ERIC M.
CHEN, KUEY-CHU
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Search completed: May 4, 2005, 16:39:31 Job time: 1042.71 secs
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RESULT 15
US-10-737-262-2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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Publication No. US20040197315A1
GENERAL INFORMATION:
APPLICANT: Stefanis, Leonidas
APPLICANT: Greene, Lloyd A.
TITLE OF INVENTION: Dopaminergic Cell Lines Stably Expressing A53T Alpha-Symuclein
TITLE OF INVENTION: and Methods of Using Same
TITLE REFERENCE: 5199-26
CURRENT APPLICATION NUMBER: US/10/737,262
CURRENT FILING DATE: 203-12-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 437
TYPE: DNA
ORGANISM: Homo
315
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 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 344
                                                                                                   ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                                                                                                                                            GAGCAAGTGACAAATGTTGGAGGAGCAGTAGTGACGGGTGTGACAGCAGTAGCCCAGAAG
                                                                                                                                                                          GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80
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                                                                     ACAGTGGAGGGAGCAGTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG
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71.82%
62.73%
51.23%
                                   ArgProSerAlaProGlnGln 107
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-Q=/cgn2_1/USPTO_spool_h/US090117715/runat_04052005_100744_25619/app_query.fasta_1.661
-Q=/cgn2_1/USPTO_spool_h/US090117715/runat_04052005_100744_25619/app_query.fasta_1.661
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOODCL=0 -LOODEXT=0
-UNITS=bits -STNART=1 -END=-1 -MATRIX=blosum62 -TEANUS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-2000000000
-USER=US09017715_0CGN 1_1_5314_@runat_04052005_100744_25619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPEJOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## ALIGNMENTS

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 CV028548 LOCUS DEFINITION
Marc Vidal Laboratory Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5180 Fax: 617 632 5399 Email: Marc Vidal@dfci.harvard.edu ORF Sequence Tag (OST) of Garteway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers PCR PRIMER: ATGGATGTCTTCAAGAAGAGGCTTCTC BACKWARD: TAGTCTCCCCCACTCTGG	Simmons, B. Sequerra, R., Bosak, S., Doucette-Stam, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 555)  Rual, J. F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,	sapiens CDNA 5' Similar to BC014098, mRNA sequence. CV028548 CV028548.1 GI:51486632 EST. Homo sapiens (human) Homo sapiens	CV028548 555 bp mRNA linear EST 20-AUG-2004 7090 Full Length cDNA from the Mammalian Gene Collection Homo

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RESULT 2
BP212912
                                 SOURCE
ORGANISM
                                                                ACCESSION
VERSION
KEYWORDS
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Plate: 11017 row: 05 column: B
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
                                                                                BP212912 Sugano cDNA library, CBR05118, mRNA sequence.
BP212912 GI:52085803
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 Homo sapiens (human)
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/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_Tib="Full Length cDNA from the Mammalian Gene
Collection"
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BP197662 Sugano cDNA libi
ADG06551, mRNA sequence.
BP197662
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@sims.u-tokyo.ac.jp.
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                                                    Homo sapiens
Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 582)
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Suzuki,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Yamashita,R.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims u-tokyo.ac.jp.
Location/Qualifiers
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Contact: Yutaka Suzuki
                                                                           Homo
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADG06551"
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/clone_lib="Sugano cDNA library,
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                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 653)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Unpublished (1999)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                     653
603030894F1 NIH_MGC_114 Homo
mRNA sequence
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/tissue_type="amygdala"
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                                                     BI836596 751
603089575F1 NIH_MGC_120 Homo
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                                                                                                                                                            GAGGCCCAGAGTGGGGGAGAC
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/rote=Torgan: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
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/mol_type="mRNA"
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'lab_host="DH10B"
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sapiens cDNA clone IMAGE:5228538 5',
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagge.llnl.gov
Plate: LLAM11575 row: e column: 19
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Tissue Procurement: Life Technologies, Inc.
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                     ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu
                                                                                               ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5228538"
/lab_host="DH10B"
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/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
/cMV-SPORT6; Site 1: Not1; Site 2: EccRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EccRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys
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Plate: LLAM13558 row: f column:
High quality sequence stop: 436.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Dr. James R. Lupski
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                                   GluAlaGlnSerGlyGlyAsp 127
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1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:6178582"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 738.
                                                                                                                                                                    /clone libs "NIH MGC 115"
//clone libs "NIH MGC 115"
//clone libs "NIH MGC 115"
//note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5752462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          lab_host="DH10B"
2.26e-58
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100.00%
98.43%
98.69%
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Matches:
Conservative:
Mismatches:
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RESULT 9
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
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BQ882072

BST 16-AUG-2002

AGENCOURT 8586140 Lupski sympathetic trunk Homo sapiens cDNA clone

IMAGE: 6195522 5', mRNA sequence.

BQ882072
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EST.
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Plate: LLAM13602 row: h column:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                               quality sequence stop: 667.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Si
NotI; Site 2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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                                                                                      /tissue_type="sympathetic trunk"
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/lab_host="DH10B"
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/clone="IMAGE:6195522"
                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                            į. .855
                                                                                                                                           'sex="male"
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RESULT 10
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Best Local Similarity:
Query Match:
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                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
11. MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence
BQ439430
                                                                                                                                                                                                                                                                                                                                                                 BQ439430 884
AGENCOURT_7911914 NIH_MGC_68
             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13197 row: k column: 11
                                                                                                                                                                                                                                                                                                        BQ439430.1
EST.
                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                              cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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quality sequence stop: 559.
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1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo
College of Medicine); available through Life
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies,
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 891)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                             Homo sapiens
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/clone_lib="NH1 MGC 68"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
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/db_xref="taxon:9606"
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Homo sapiens cDNA clone IMAGE:6057784
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 903)
                                                                                                                                                                    Homo sapiens
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BG286466.1 GI:13039369
                                                                                                                                                               mRNA sequence.
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                                                                                   Homo sapiens (human)
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/clone_lib="WIH_MGC_68"
/clone_lib="WIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies."
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/db_xref="taxon:9606"
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TITLE
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National Institutes of Health, M
Unpublished (1999)
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Tissue Procurement: ATCC
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mRNA sequence.
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Location/Qualifiers
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Plate: LLAM10366 row: k column:
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                                                                                                                        GluAlaGlnSerGlyGlyAsp 127
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Syste_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_1.7 %b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11656 row: m column: 06
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be
                ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100
                                                                           GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys
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ACCGTGGAGGAGGAGGACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: !
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:5260589"
/tissue_type="hippocampus"
/lab_host="DH10B"
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10682 row: a column: 13
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National Institutes of Health, M
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602674249F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4796820
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone libe"NIH MGC 96"
/clone libe"NIH MGC 96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI_XhoI (9tcgae); Oligo-dT primed using primer (9tcgae); Oligo-dT primed using primer structure of the structure of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 617)
                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 617.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10674 row: e column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGCCCAGAGTGGGGGAGAC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGTGGAGGAGGAGGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCCATCTGCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAAGAGGAAGTGGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
                               /note=Torgan: brain; Vector: pBluescriptR (modified pBluescript RS+); Site 1: BamHI; Site 2: SalI-XhoI pBluescript RS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this
                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                      clone
                                                                                                                                                                                                                                                                         tissue_type="hypothalamus"
                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                        lab host="DH10B"
                                                                                                                                                                                                                                                                                               clone="IMAGE: 4793833"
                                                                                                                                                                                                                                                                                                                                                                                      .617
                                                                                                                                                                                                                                 11b="NIH_MGC_96"
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Alignment Scores:

Qy 101 ArgProSerAlaProGlnGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120	Qy 81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLySGluAspLeu 100	Qy 41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60	US-09-017-715A-2 (1-127) x BG707764 (1-617)	97.54% Indels: 4 Gaps:	nt Similarity: 99.21% Conservative: Local Similarity: 97.64% Mismatches:	595.00 Matches:		1e-57
Db 358 AddCCATCTGCCCCCCAACAGAGGGTGTGGCATCCAAAGAGAAAGAGAAGTGGCAGAG 417  Qy 121 GluAlaGInSerGlyAsp 127	298 ACCGTGAGAGAGCGGAGAAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 101 ArgProSerAlaProGlnGlnGluGJyGluAlaSerLysGluIySGluIyGluValAlaGlu	178 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGCCCAAAGACCAAGGACAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAAGACCAAGACCACAAGACCAAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCACC	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPhetysLysGlyPheSerIleAlalysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21%	re: cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 4	d. No.:  1e-57  Matches: 124  cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1  ry Match: 1
358 AGGCCATCTGCCCCCAACAGGAGGTGTGGCATCCAAAGAGAAAGAGAAGTGGCAGAG 121 GluAlaGlaSerGlyGlyÆsp 127	298 ACCGTGGAGGAGGAGAACATCGCGGTCACCTCCGGGGTGCGCAAGGAGACTTG 101 ArgProSerAlaProGlnGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu	61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 62 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGCCACGAGGCTGAGCACCAAG 81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 61 [	1 MetAspValPheLysLysGlyPheSerIleAlaJysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Indeals: 0  ry Match: 97.54% Indeals: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	re: cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 97.54% Indels: 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalPhetystysGlyPheSerIleAlatystysGlyValValValGlyAlaValGlu	dd. No.:  1e-57  re: 595.00  Matches: 124  Conservative: 2 t Local Similarity: 97.54%  Mismatches: 1 ry Match: 4  O9-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGluValAvalGlu
358 AGGCCATCTGCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAGAAAGAGGAAGTGGCAGAG	298 ACCGTGGAGGAGGAGGACTTGCGGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu	178 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCTTACCTCAGTGGCCAAGAACAAGACCAAG 61 GIUGINALASNALAVALSETLYSALAVALVALSETSETVALASNTHYVALAGAGACCAAG 61 GIUGINALASNALAVALVALSETSETVALASNTHYVALAGAGACCAAG 61 GIUGINALAGSAGACCAGCGGTGAGCAGCTGTGGTGACACTGTGGCCACAAG 61 GIUGINALAGSAGACGCGGTGAGCAGCGTTGGTGAGCAGCACCAAG 62 GAGCAGCCAACGCGGTGAGCAGGCTGTGGTGAGCACCACAAG 63 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 64 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAsgAGAAGAGGAAGCTTG 65 ACCGTGGAGGAGGCGGAGAACATCGCGGTTGTGCCGCAAGAGGAAGTGGCAGAG 66 ThrValGluGlyGluAlaSerLysGluLysGluLysGluCluValAlaGlu 67 ThrValGluGlyGluAlaSerLysGluLysGluLysGluCluValAlaGlu 68 ThrValGluGlyGluAlaSerLysGluLysGluCluValAlaGlu 69 ACCGTGACCCCCCAACAGGAGGGTGTGGCATCCAAAGAGAAAAGAGGAAAGTGGCAGAG	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ry Match: 97.54% Indeals: 0 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalphetystysGlyPheSerIleAlatystysGlyValValValGlyAlaValGlu 58 ATGGATGTCTTCAAGAAGGGCTTCTCCCATCCCCAAGGAGGCGTGGTGGGTG	re: cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 97.54% Indels: 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLyeLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	d. No.:  1e-57  Matches: 124  cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 1 4  Op-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalphelystysGlyPheSerIleAlalystysGlyValValGlyAlaValGlu
	298 ACCGTGGAGGAGGGCGGAAAATCGCGGTCACCTCCGGGTGGTGCGCAAGGAGGACTTG 101 ArgProSerAlaProSinGlnGlnGlyGlnAlaSerLysGluLysGluGluValAlaGlu 111	178 GGAGCCAAGACCAAGGACAAGACGAAGACCAAGACCAAGACCAAGACCAAGACCAAGCACAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAAGACCAAGACCAAGACCAAGACCAAGACCACC	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0  0  0  0  0  0  0  0  0  0  0  0  0	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ty Match: 97.54% Indels: 0  ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalphelystysGlyPheSerIleAlalysLysGlyValValGlyAlaValGlu	re: cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	dd. No.:  1e-57  re: 595.00  Matches: 124  cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 4 Gaps: 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
		178 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 61 GJUGJAASNAJAVAJSETSETSAJAVAJVAJSETSETVAJASNTHYVAJAJATATLYS	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValQlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0  99-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 t Local Similarity: 97.54% Indeals: 0 exy Match: 97.54% Indeals: 0  09-017-715A-2 (1-127) x BG707764 (1-617) 1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 58 ATGGATGTCTTCAAGAAGGGTTCTCCATCGCCAAGGAGGGGTGTGGTGGCGTGGGTGG	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.54% Mismatches: 1  ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	d. No.:  1e-57  Fength:  1e-17  re:  595.00  Matches:  124  Cent Similarity:  99.21%  Conservative:  2 t Local Similarity:  97.54%  Mismatches:  1  Mismatches:  1  ry Match:  1  MetaspvalpheLysGysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 		178 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCCAGTGGCCCAGAAGACCAAG 61 GluGlnAlasnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 t Local Similarity: 97.54% Indels: 0 ry Match: 97.54% Indels: 0 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MethspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.54% Mismatches: 1  ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysGlyPheSerIleAlaLysLysGlyValValValGlyAlaValGlu	d. No.:  1e-57  Matches:  124  cent Similarity:  99.21%  Conservative:  2 t Local Similarity:  97.54%  Mismatches:  1 metaspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyPheSerIleAlaLysLysGlyValValGagaga  09-017-715A-2 (1-127) x BG707764 (1-617)  1 metaspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyPhalaValGlu   1 metaspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGagaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGa
238 GAGLAGGCCAAGAGCGAGGCTGTGGTTGAGCGGTCAACACTGTGGCCAACAAGAGAGGCCAACAAGAGAGGCCAACAAGAGAGGCCAACAA	238 GAGCAGGCCAACGCGGTGAGCGAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG	178 GGAGCCAAGACCAAGGAGTGTTGTTACAGAGCCTCAGTTGGCCGAGAAGACCAAG	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match:  97.54%  Gaps:  0  0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ty Match: 97.54% Indels: 0  ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalphelystysGlyPheSerIleAlalysLysGlyValValGlyAlaValGlu	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ry Match: 97.54% Indels: 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MethspvalpheLysLysGlyPheSerIleAlaLysLysGlyValvalGlyAlaValGlu	dd. No.:  1e-57  Length:  7e:  595.00  Matches:  124  Conservative:  2 t Local Similarity:  97.54%  Mismatches:  1  Mismatches
61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys	61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 		1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match: 97.54% Indels: 0  4 Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetaspvalPhetystysGlyPheSerIleAlatystysGlyValValGlyAlaValGlu	cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.54% Mismatches: 1 ry Match: 97.54% Indels: 0 cry Match: 4 Gaps: 0 cop-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	re: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.64% Mismatches: 1  t Conservative: 2  conservative:	dd. No.:  1e-57  re: 595.00  Matches: 124  cent Similarity: 99.21%  t Local Similarity: 97.64%  ry Match: 1
41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys	41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys		1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match: 97.54% Indels: 0  Gaps: 0  97.54% Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ry Match: 97.54% Indels: 0 ry Match: 4 Gaps: 0 09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspvalPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ry Match: 97.54% Indels: 0 cy Match: 4 Gaps: 0 cy Match: 4 Gaps: 0 cy Match: 1 cy Match: 1 cy Match: 1 cy Match: 1 cy Match: 97.54% Indels: 0 cy Match: 97.54% Indels: 0 cy Match: 1 cy Matches: 1 cy Ma	d. No.:   1e-57
118 AAGACCAAGCAGGGGTGACGAAGCAACCAAGGAAGGACGACCAAGGAGGACGACCAAGCAAGGAGG	118 AAGACCAAGCAGGGGTGACGAAGCAGCAGCAAGACCAACGAAGGACGAGCAGGAGG	118 AAGACCAAGCAGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGT	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match: 97.54% Indels: 0  4 Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Conservative: 2   Conservati	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.54% Mismatches: 1  ry Match: 97.54% Indels: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	d. No.:       1e-57       Length: 617         re:       595.00       Matches: 124         cent Similarity:       99.21%       Conservative: 2         t Local Similarity:       97.64%       Mismatches: 1         ry Match:       4       Gaps: 0         op-017-715A-2 (1-127)       x BG707764 (1-617)         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlu         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlu         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlu         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlu         1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlu
21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal	21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal	21 LYSThrLySGlnGlyValThrGluAlaAlaGluLySThrLySGluGlyValMetTyrVal 	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	-09-017-715A-2 (1-127) x BG707764 (1-617)  1 MecAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	ry Match: 97.54% Indels: 0  Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu	Cent Similarity: 99.21% Conservative: 2 t Local Similarity: 97.64% Mismatches: 1 ty Match: 97.54% Indels: 0 cry Match: 4 Gaps: 0 09-017-715A-2 (1-127) x BG707764 (1-617) 1 MetAspValPheLysLysGlyPheSerileAlaLysLysGlyValValGlu	re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.64% Mismatches: 1  ry Match: 97.54% Indels: 0  ry Match: 4 Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyUalValGlu	d. No.: 1e-57 Length: 617  re: 595.00 Matches: 124  cent Similarity: 99.21% Conservative: 2  t Local Similarity: 97.64% Mismatches: 1  ry Match: 97.54% Indels: 0  ry Match: 4 Gaps: 0  09-017-715A-2 (1-127) x BG707764 (1-617)  1 MetAspValPhelysLysGlyPheSerIleAlaLysLysGlyValValGluu  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 32 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 33 LysThrLysGlnGlyValThrGluAlaGluLysThrLysGluGlyValMetTyrVal 34 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 35 GAGCCAAGGAGCAGGAGAATGTTGTACAGAGGAGGAGCTCAGTGGCCGAGAGACCAAG 36 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 36 GAGCCAAGGAGAATGTTGTACAGAGGTGACCTCAGTGGCCGAGAGACCAAGGACCAAG 37 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 38 GAGCAGGCCAAGGAGGAGGAGGAGGTGGTGGGGCAAGGAGACCACTGGGGGTGAGGAGGAGGACGACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 31 LysThrLysGluGlyValThrGluAlaAlaGluLysThrLysGluGlyValThrGrangCAAGGAAGACCAAGGAGGGGTCATGTATGTG 41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 41 GlyAlaLysThrLysGluAsnValGluGluGluGluGluGluGluGluGluGluGluGluGlu	58 ATGARIGICTICADAGAAGGCCTTCTCCATCGCCAGGAGGCCGTGGTGGTGGTGGTGGTGGGTG		(1-127) x BG707764	ry Match: 97.54% Indels: Gaps: 09-017-715A-2 (1-127) x BG707764 (1-617)	cent Similarity:       99.21%       Conservative:         t Local Similarity:       97.64%       Mismatches:         ry Match:       97.54%       Indels:         Gaps:       6         09-017-715A-2       (1-127)       x BG707764       (1-617)	re: 595.00 Matches: cent Similarity: 99.21% Conservative: t Local Similarity: 97.64% Mismatches: ry Match: 97.54% Indels: 4 Gaps: 09-017-715A-2 (1-127) x BG707764 (1-617)	d. No.:       1e-57       Length:         re:       595.00       Matches:         cent Similarity:       99.21%       Conservative:         t Local Similarity:       97.64%       Mismatches:         ry Match:       4       Indels:         6aps:       Gaps:

Search completed: May 4, 2005, 13:46:32 Job time: 5788.07 secs

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-MODBLI-frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/USO9017715/runat_04052005_100743_25600/app_query.fasta_1.661
-Q=/cgn2_1/USPTO_spool_h/USO9017715/runat_04052005_100743_25600/app_query.fasta_1.661
-DB=N Geneseq -QFMT=fastap -SUFTIX=rung -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START1 = LNDE-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_GCGN 1_1_703_@runat_04052005_100743_25600 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ach73352 Human gen
Aax04876 Human gam
Adt46476 Bacterial
Acn91507 Breast ca
Adc08755 Rice DNA
Adc08252 Rice DNA
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Adc39175 Novel hum
Adq89903 Antagonis
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Adq88477 Human tum
Aax00463 Human typ
Adp21328 Gene ADCY
Adf74204 Human nov
Adc30279 Human nov
Adc30367 Human sof
Abq81847 Bifidobac
Aak76569 Human imm
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Adh54342 Human SNC
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Ab104107 Drosophil
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### ALIGNMENTS

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RESULT 1
AAF217S
IID AAF27
XX AAF27
XX AAF27
XX AAF2
XX AAF2
XX Y
DT 27-N
DE Huma
XX H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antivital; antiallergic; hepatotropic; antidiabetc; antiinflammatory; antiuncer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease, allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                                                  08-MAR-2000; 2000WO-US005881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast and ovarian cancer associated antigen gene SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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ID 172.

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RESULT 2
ACH15493
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Pred. No.:
Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are Equences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; antiungal; antiparastic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly compressive and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly compressive and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment confinement disorders e.g. Addison's diabetes mellitus, Crohn's classes, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; and constitution as myocardial accidents, wound healing; and constitutions and disorders such as myocardial accidents.
             30-JUL-2001; 2001US-00918995
                                              30-JUL-2001; 2001US-00918995
                                                                                                               US2003073623-A1
                                                                                                                                                                                genome
                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                 Human adult brain cDNA #2705.
                                                                                                                                                                                                                                                                                                   ACH15493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 478 BP; 118 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 609; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                               17-APR-2003
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                  13-OCT-2003
                                                                                                                                                                                                                                                                                                                                    ACH15493 standard; cDNA; 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological diseases such as cerebral anoxia and epilepsy; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                                                                                                                                           ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                       GluGluAlaGlnSerGlyGlyAsp
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Conservative:
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ADM668A

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XX ADM6

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XX Homc

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XX DE Huma

XX Homc

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide comprising any one of CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was Cd determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to CC are useful in diagnostics as expressed sequence tags (EST) for CC identifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide Sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of CC for chromosome and gene mapping, in the recombinant production of CC is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data cobtained in electronic forms part of the printed specification, but was obtained in electronic forms part of the printed specification, but was compared to the compared of the sequence of the sequence.
                                                                                                                                                                                                                                      human; adipocyte specific; gene; ds; adipose tissue; high mobility group I-C protein; HMGI-C; obesity; le adipogenesis; hypertension; cardiovascular disease; antidiabetic; hypotensive; gamma synuclein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Human homologue of murine adipocyte specific gamma synuclein DNA Seq 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
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(LABA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GluGluAlaGlnSerGlyGlyAsp
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JONES L W.
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                                                                                                                                                                                                                                                                                                         ds; adipose tissue; anti-obesity; HMGI-C; obesity; leptin; ob; diak
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Matches:
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29-JUL-2003; 2003WO-US023684

05-FEB-2004. WO2004011618-A2

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ARESULT 4
AAV42669
ID AAV4
XX AAV4
XX O9-N
XX Huma
XX Huma
XX Brea
XX Brea
XX Homc
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-017-715A-2_COPY_120_127 (1-8) x ADM66887 (1-488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is epistatic to leptin, furthermore, it refers to the obgene where an autosomal recessive trait is linked to obesity and diabetes. The present invention describes performing differential gene expression analysis between the white adipose tissue (WAT) or stromal vascular tissue (SVT) of any two different mice selected from a group consisting of wild-type, HMGI-C-/-, ob/ob, or HMGI-C-/-, ob/ob genotype mice. Accordingly, using this method novel nucleotides and the encoded proteins thereof were identified that are adipocyte specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes, obesity, hypertension and cardiovascular disease, as well as screening for compounds that can modulate or prevent adipogenesis and treat diabetes or obesity. These compositions exhibit anorectic, antidiabetic and hypotensive activities. This polynucleotide sequence is a human homologue of a murine adipocyte specific DNA sequence of the invention.
   WO9833915-A1
                                                                                                                                                                                                                                                     Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis; therapy; genetic marker; ds.
                                                                                                                                                                                                                                                                                                                                                      Human breast
                                                                                                                                                                                                                                                                                                                                                                                                                   8661-AON-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV42669 standard; cDNA; 550
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12-JUN-2003; 2003US-0478206P.
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                                                                                                                                                                                                                                                                                                                                                   cancer specific gene 1 (BCSG1) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                     Location/Qualifiers
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Matches:
Conservative:
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RESULT 5
AAA3940
ID AAA33
XX AAA3
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human breast cancer specific gene 1 (BCSG1), and includes an open reading frame for a 14.2 kDa protein (see AAMG3123). It was isolated from a breast cancer cDNA library following an BST search for novel genes differentially expressed in breast cancer versus healthy breast tissue. The clone is deposited at ATCC 97175 and ATCC 97856. A gradient and stage specific BCSG1 expression has been demonstrated from virtually no detectable expression in normal or benign breast to low level and partial expression in low grade in situ breast carcinoma and high expression in infiltrating malignant breast carcinomas. BCSG1 is useful as a breast cancer progression marker. Recombinant vectors and host cells useful for recombinant production of BCSG1 polypeptides (including epitope-bearing malignant).
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                       amyloid-like
                                                                                                                                                                                                                                                            Human; ADA2; cytostatic; gene therapy; treatment; cancer;
                                                                                                                                                                                                                                                                                                                             Human HBGBA67A DNA.
                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA39470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA39470 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 550 BP; 132 A; 145 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides) are provided. BCSG1 polynucleotides, polypeptides and antibodies can be used for the detection of breast cancer cells or breast cancer metastasis, and to develop methods for the clinical management and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA clone corresponds to the transcript of the newly identified human breast cancer specific gene 1 (BCGG1), and includes an open read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ji H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                       protein;
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                              /product= "HBGBA67"
                                                          /*tag=
                                                                                                                     Location/Qualifiers
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Indels:
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Best Local Similarity:
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          05-JUN-2000;
05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
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                                                                                                 30-MAY-2001; 2001WO-US010838
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                          Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancero
                                                                                                                                                                                                                                           Breast cancer
                                                                                                                                                                                                                                                                                                          ABL63343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 550 BP; 132 A; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity. This sequence encodes a polypeptide derived from the h
HBGBA67X clone which is an amyloid-like protein found in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 27-28;
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P-PSDB; AAY87779.
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                                                                                                                                                                                                                                                                                     ABL63343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s invention describes a novel polynucleotide (I) encoding human ADA2. products of the invention have cytostatic activity and can be used gene therapy. (I) is useful for treating cancer; as primers and bes for isolating full length cDNA and genes having similar biological ivity. This sequence encodes a polypeptide derived from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide encoding human AD2 is useful for treating cancisolating cDNAs and genes having similar biological activity.
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                                                                                                                                                                                                                                                                                                                                                                GluGluAlaGlnSerGlyGlyAsp
                                                                                                                                                                                                                                                                                                           standard;
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          2000US-0209473P.
2000US-0209531P.
2000US-0233131P.
2000US-0233617P.
2000US-0234040P.
2000US-0234034P.
2000US-0234052P.
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                           related
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                                                                                                                                                                                               therapy; antineoplastic; Wilm's
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41.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                          gene
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                           antitumour; cancerous;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                                                 tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer
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Alignment S Pred. No.:

Sequence

132

P 145

ű 192

G.

81 T; 0 ₽

0 Other;

Percent Similarity:

55.4 41.00 100.00%

Conservative:

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CC neoplastic agent. The method involves exposing cells to a chemical agent (to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an CC anti-neoplastic agent, and can be used for producing a product which is CC the data collected with respect to the anti-neoplastic agent as a result CC fMI, and the data is sufficient to convey the chanical structure and/or properties of the agent. MI can be used in the treatment of cancer such CC as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell; cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
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03-OCT-2000;
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03-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                       Screening for anti-
agent to be tested
in expression of a
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28-SEP-2000;
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26-SEP-2000;
                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                                                                                                                                                                                                                                                         present invention describes a method (M1) for screening for an entire marked involves exposing cells to a chemical
                                                                                                                                                                                                                                                                                                                                                                                                                        2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PE,
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2000US-023571P.
2000US-023571P.
2000US-0235840P.
2000US-0235863P.
2000US-0236032P.
2000US-0236034P.
2000US-0236034P.
2000US-0236109P.
2000US-023611P.
2000US-0236842P.
2000US-0236842P.
2000US-0237173P.
2000US-0237278P.
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2000US-0235280P.
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ga change
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Best Local Similarity: Query Match:

100.00%

useful for the diagnosis of SSDs, or susceptibility to SSDs,

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The present sequence is that of cDNA encoding the Glu-110 isoform of CDNA man gamma-synuclein. The invention relates to an isoform of gamma-CC synuclein that is caused by an A/T single nucleotide polymorphism (SNP) CC at position 329 of the gamma-synuclein coding sequence. This SNP causes a CC glutamic acid to valine change at amino acid position 110 of gamma-CC synuclein, and is associated with an increased susceptibility of cindividuals to schizophrenia spectrum disorders (SSDS). This is the first CC time that a genetic component of SSDs has been identified, and provides a CC potential target for diagnosis and treatment of schizophrenia. Gamma-CC synuclein polypeptides, especially those containing the E110V mutation, CC are used in a claimed method of screening for agonist compounds useful for the CC claimed method of screening for agonist or antagonist compounds. An CC claimed method of screening for agonist or antagonist compounds. An CC claimed method of screening for agonist or antagonist compounds. Of CC sequence is used for the discrimination of an SNP at position 329 of the CC coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for compounds for treating or interfering with the onset of Schizophrenia Spectrum Disorders, by detecting interactions of candidate compounds with the gamma-synuclein polypeptide.
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DB; ABP54932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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The present sequence is that of cDNA encoding the Val-110 isoform human gamma-symuclein. The invention relates to an isoform of gamma symuclein that is caused by an A/T single nucleotide polymorphism at position 329 of the gamma-symuclein coding sequence. This SNP c glutamic acid to valine change at amino acid position 110 of gamma
                                                                                          Screening for compounds for treating or interfering with the onset of Schizophrenia Spectrum Disorders, by detecting interactions of candidate compounds with the gamma-synuclein polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification of a polynucleotide encoding gamma-synuclein of the occurrence of the SNP at position 329. A transgenic for the study of SSDs is also claimed
                                                                     Disclosure; Page; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                   variation
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schizophrenia; neuroleptic; mutant; gene; ss.
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                                                                                                                                           P-PSDB;
                                                                                                                                                                            Roberts RC,
                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
(UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                15-MAR-2001; 2001US-0276306P
                                                                                                                                                                                                                                                                       14-MAR-2002; 2002WO-EP002872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local S
y Match:
New isolated protein and nucleic acid molecules, and therapeutic purposes, e.g. for treating generouscular dystrophy or cystic fibrosis.
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                                                                                                        P-PSDB; ABW02024.
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96US-00705771.
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The invention relates to an isolated human polypeptide. polynucleotides, agonists or antagonist are useful for o

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30-AUG-1996;
14-OCT-1999;
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                                                                                                                     New human polypeptides and polynucleotides, useful for diagnosing or treating genetic diseases such as muscular dystrophy or cystic fibrosis, hypertension, asthma, depression or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human amyloid like protein cDNA.
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                                                                           Claim 18;
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                                                                         ID NO 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                        GENOME SCI INC.
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96US-00705771.
99US-00417540.
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/product= "Amyloid like protein"
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                                                                                                                    This sequence represents the gene encoding a novel human synuclein family member designated persyn. The sequence is useful for screening, diagnosing or monitoring cancer (especially breast or skin cancer), neurodegenerative disorders or skin disorders and for identifying cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension, angina pectoris, myocardial infarction, ulcers, asthma, allergies, psychoses, depression, migraine, vomiting, benign prostatic hypertrophy or osteoporosis. The polypeptides and polynucleotides are useful for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vector. The present sequence represents cDNA encoding human amyloid like protein.
                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; synuclein; persyn; diagnosis; neurodegenerative disorder; breast; skin; intermediate filament damage; ss.
                                                                                   Sequence 720
                                                                                                                                                                              Claim 29; Page 16-17; 39pp; English
                                                                                                                                                                                                          disorders.
                                                                                                                                                                                                                  New synuclein protein (persyn) and gene, useful in assays for screening, diagnosing or monitoring cancer, neurodegenerative disorders or skin
                                                                                                                                                                                                                                                                      WPI;
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(UYSA-) UNIV ST ANDREWS
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DB; AAY07271.
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                                                                                                          intermediate filament damage
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RESULT 12
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14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-032967P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325149P.
              The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian of eacher). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain and central optical management and treatment of the management cancer (e.g. brain and central optical management and treatment of the management cancer (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain and central optical management and treatment of the management and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
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                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 411; 481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer patient.
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Morrisey MP, Olandt PJ, Sen A, Vieby PO,
u K, Schmandt RE, Zhao X, Glatt K;
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), Mills GB;
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RESULT 13
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08-NOV-2001;
08-NOV-2001;
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                                                                                                                                                 Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
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Chromosome 10; gene; ss.
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Alzheimer's disease; neuroprotec
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GEN HOSPITAL CORP.
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; 2001US-0336929P.
; 2001US-0338010P.
; 2001US-0338363P.
; 2001US-0337052P.
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, Mullin KM,
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neuroprotective;
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Sampson AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDE; KNSL1; LIPA; nootropic; gene ti
                                                                                                                                                                                                                                                                                                  Wang X, T
Blacker DL;
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                                                                                                                                                                                                                                                                                                                              Bertram
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Claim 84;

Page

740;

848pp; English

Determining a predisposition for or the occurrence of neurodegenerative disease, particularly Alzheimer's disease, comprises determining the presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6

2004-060538/06

present invention relates to a method (M1) for determining

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25-OCT-2001; 2001US-0348065P.
02-NOV-2001; 2001US-0336983P.
08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from upa (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulindegrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid lypase), and TWRRSF6 (Thmour Necrosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10, M1 is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly
                                                                                        Becker KD,
Bertram L,
                                                                                                                                                                                                                                                                                                                           US2003224380-A1
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                                                                                                                                                                                                                                                                                                                                                                                                 human; neurodegenerative disease; urokinase plasminogen activator; uPA;
gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human SNCG
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                                                                                                                                                                                                                                                                         25-OCT-2002; 2002US-00282174.
                                                                                                                                                                                                                                                                                                                                                                         gamma-synuclein; SNCG; insulin degrading enzyme; IDE;
kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's c
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                                                                                         Saunders
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Claim 84;

SEQ ID NO 469; 205pp; English.

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56.
P-PSDB; AAO13847.
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac
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                                                                                                                                                 Claim 1; SEQ ID NO 13838; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                      polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this pateent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                            Sequence 783 BP; 187 A; 232 C; 237 G; 127 T; 0 U; 0 Other;
471 GAGGAGGCCCAGAGTGGGGGAGAC 494
                          1 GluGluAlaGlnSerGlyGlyAsp 8
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-Q=/cgn2 1/USPTO_spool h/US09017715/runat_04052005 100745 25632/app_query.fasta_1.661
-Q=/cgn2 1/USPTO_spool h/US09017715/runat_04052005 100745 25632/app_query.fasta_1.661
-DB=Issued_patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715 @CCN 1 116 @runat 04052005 100745 25632 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4. /cgn2_6/ptodata/1/ina/B_COMB.seq:*
5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6. /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-417-540-1

US-09-949-016-1915

US-09-949-016-442

PCT-US95-08295-1

US-09-949-016-3084

US-09-949-016-3085

PCT-US94-09789-1

US-09-949-016-3086

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US-08-705-771-1
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Sequence 1, Application Patent No. 6054289 TELEPHONE: 973-994-170
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/70
FILING DATE: August 30, 1996
CLASSIFICATION: 536 GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji, APPLICANT: Jian Ni and Jing-Shan Hu TITLE OF INVENTION: Human Genes, Sequences and TITLE OF INVENTION: Expression Products CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: STREET: 6 BECKI CITY: ROSELAND ADDRESSEE: CARELLA, BYRNE, BAIN, GIL ADDRESSEE: CECCHI, STEWART & OLSTEIN Application US/08705771 NEW JERSEY 6 BECKER FARM ROAD USA 973-994-1700 US/08/705,771 August 30, 1996 ON: 536 325800-346 (PF196) BAIN, GILFILLAN

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.: 550 base pairs
.:rPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DN°
US-08-705-771-1
Alignmen*
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US-09-417-540-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                          Sequence 1, Application Patent No. 6639052
GENERAL INFORMATION:
          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM Ps/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION UMBER: US/09/417,540
FILING DATE: 14-OCT-199
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                    APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji, TillE OF INVENTION: Human Genes, Sequences and Expression Products
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
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CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         Application US/09417540
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Best Local Similarity:
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Sequence 1915, Application US/09949016
Patent No. 6812339
GENERRAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEPAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 1:
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No.:
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FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1915
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1915
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Alignment Scores:
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Best Local Similarity:
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                                               SEQ ID NO 442
LENGTH: 720
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                     Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 442,
                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PRIOR SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity:
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US-09-017-715A-2 (1-127) x PCT-US95-08295-1 (1-786)
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DB:
                                                                                                                  Alignment Scores:
                                                                                                                                                 PCT-US95-08295-1
                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08295
FILING DATE: 30-JUN-1995
CLASSIFICATION:
INFORMATION PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-08295-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9508295 GENERAL INFORMATION:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                           TOPOLOGY:
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MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu

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PATERIT NO. 681239

| PATERIT NO. 681239
| GENERAL INFORMATION: ENTER AL. APPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES |
| TITLE OF INVENTION: UNIMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR APPLICATION NUMBER: 60/237,768 |
| PRIOR APPLICATION NUMBER: 60/237,768 |
| PRIOR APPLICATION NUMBER: 60/231,498 |
| PRIOR FILING DATE: 2000-09-08 |
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US-09-949-016-58
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US-09-949-016-58
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SEQ ID NO 58
LENGTH: 1543
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FastSEQ for Windows Version
                               GlyAlaLysThrLysGluAsnValValGinSerValThrSerValAlaGluLysThrLys
                                                                                                 AAAACCAAACAGGGTGTCGCAGAAGCAGCAGCAGGAAAGAAGAGGGTGTTCTCTATGTA
                                                                                                                                                                                                                                                MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
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GGCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAACAGTGGCTGAGAAGACCAAA
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LENGTH: 1543
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Patent No. 6812339
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PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SCOTD MARE: FASLSEQ for Windows Version 4.0
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ORGANISM: Human
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 GGCAAGAATGAAGAAGGAGCCCCACAGGAA 376
                                                                              ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu
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                                                    ACAGTGGAGGGAGCAGTTGCAGCAGCCACTGGCTTTGTCAAAAAGGACCAGTTG
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; ORGANISM: Human
US-09-949-016-3085
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LENGTH: 1543
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                            Sequence 1, Application PC/TUS9409789 GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                 APPLICANT: The Regents of the University of California TITLE OF INVENTION: NOVEL COMPONENT OF AMYLOID IN TITLE OF INVENTION: ALZHEIMER'S DISEASE AND METHODS FOR NUMBER OF SEQUENCES: 12
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                                                                E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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Sequence 3086, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
FILE REFERENCE: CL001307
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: cDNA for NACP
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EDNESS: single
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RESULT 11
US-09-949-016-3087
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; ORGANISM: Human
US-09-949-016-3086
                                                                                                FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3087
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3087, Application US/09949016 Patent No. 6812339
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2000-04-14
ORGANISM: Human
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US-09-949-016-2926
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Best Local Similarity:
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Query Match:
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                                                  US-09-017-715A-2 (1-127) x US-09-949-016-2926 (1-703)
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                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISSASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PHILING DATE: 2000-10-03
PRIOR PHILING DATE: 2000-10-03
PRIOR PHILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,488
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2926, App
Patent No. 6812339
                                                                                                                                                                                                                                                                               SEQ ID NO 2926
LENGTH: 703
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GAGCAAGTGACAAATGTTGGAGGAGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAG
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
Patent NO. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2232
RESULT 14
US-09-949-016-13657
; Sequence 13657, A
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Query Match:
DB:
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US-09-513-999C-2232
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                                                                                                                                                                                                                                                                                                                                                                                                   TERGTH: 313
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: 136..312
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Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 117
OTHER INFORMATION: m=a
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                                                                                                                        21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40
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                                                                                                                                                                      1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
                                                                    GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThr 59
                                                                                                       GAACAGGCCTCACATCTGGGAGGAGCTGTGTTCTCTGGG---
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 Application US/09949016
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Matches:
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                                                                                                       255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(8607)
; OTHER INFORMATION: n = A
US-09-949-016-13657
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                        Sequence 12184, Application US/09949016
Patent No. 6812339
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12184
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PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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2888	38 ACCCCACAGTTTGTCCAGCTGTTCTGTTGTGTTTTGTCCTGACCGCCCCCAACACCTCGAG 2947	
4.	41GlyAlaLysThrLysGluAsnValVa 49	
2948	18 GGAGGTCTGGGCTGACAGCTCCATTTCCTCCCCAGGAGCCAAGACCAAGGAGAATGTTGT 3007	
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3067	57 CCTGGGGCTCCTGCATCCTAGTGCTGGGGCTCAAACCTAGAGTCCTGCCTTACCCCCAAC 3126	
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-UNITS=bite -STRATF1= -END=-1 -MATRIX=blosum62 -TTR_MNS=human40.cdi -LIST-45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09017715_GCGN 1 1 703 @runat 04052005_100743_25600 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                          Score
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019
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Match
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geneseqn1990s:*
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Ygapext
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      AAV42669
AAA39470
ABL63343
ABV73813
AAD63568
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7.0
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809.955 Million cell updates/sec
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Aav42669 Human bre
Aaal39470 Human HBG
Abl63343 Breast ca
Abv73813 Human gam
Aad63568 Human amy
                                                                                                                          Description
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BX39864 ADB37445 ADP44633
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ADO24508 ADP44624
AAD14354 AAD44409
ABT42008 ABT91875
DA57841 ADR98806
ADM66886 AT51183
AAX29998
CH15493
ADE43864
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## ALIGNMENTS

AAV42669;

AAV42669 standard; cDNA; 550 BP.

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RESULT 1
AAV42669
ID AAV4
XX AAV4
XX AV4
XX DS Huma
XX Brea
XX Brea
XX Homc
XX Hom
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cancer specific gene 1 (BCSG1) cDNA.
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                                                            (HUMA-) HUMAN GENOME SCI INC
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA clone corresponds to the transcript of the newly identified CC human breast cancer specific gene 1 (85G1), and includes an open reading CC frame for a 14.2 kDa protein (see AAW63123). It was isolated from a CC breast cancer cDNA library following an EST search for novel genes and CC differentially expressed in breast cancer versus healthy breast tissue. CC The clone is deposited at ATCC 97175 and ATCC 97856. A gradient and stage CC especific BCSG1 expression has been demonstrated from virtually no CC detectable expression in normal or benign breast to low level and partial CC expression in low grade in situ breast carcinoma and high expression in CC infiltrating malignant breast carcinomas. BCSG1 is useful as a breast CC cancer progression marker. Recombinant vectors and host cells useful for CC recombinant production of BCSG1 polypeptides (including epitope- bearing CC polypeptides) are provided. BCSG1 polypeptides (including epitope- bearing CC antibodies can be used for the detection of breast cancer cells or breast CC cancer metastasis, and to develop methods for the clinical management and CC cancer metastasis, and to develop methods for the clinical management and CC cancer metastasis, and to develop methods for the clinical management and CC cancer metastasis, and to develop methods for the clinical management and CC cancer metastasis, and to develop methods for the clinical management and CC cancer metastasis.
AAA39470;
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                                  AAA39470 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match:
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                                                                                                                             GluAlaGlnSerGlyGlyAsp 127
                                                                                                                                                                                                      ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGCCCAGAGTGGGGGAGAC
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                       Alignment
                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel polynucleotide (I) encoding human ADA2. The products of the invention have cytostatic activity and can be used for gene therapy. (I) is useful for treating cancer; as primers and probes for isolating full length cDNA and genes having similar biological activity. This sequence encodes a polypeptide derived from the human HBGBA67X clone which is an amyloid-like protein found in breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ADA2;
amyloid-like
                                                                                                                                                                                                                                                                                                                                               Sequence 550 BP; 132 A; 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 27-28; 54pp; English.
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)B; AAY87779.
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ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu
                                              GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys
                                                                                              GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys
                                                                                                                                           LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal
                                                                                                                                                                             MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
                                 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG
                                                                                GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG
                                                                                                                                cytostatic; gene therapy; treatment; cancer;
protein; ss.
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12. .395
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Matches:
Conservative:
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ACCGTGGAGGAGGAGGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG

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18-SEP-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001WO-US010838
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The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC properties of the agent. M1 can be used in the treatment of cancer such
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1680; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Augustus M, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter
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Sequence 550 B₽; 132 A; 145 Ç 192 <u>ი</u> 81 Ŧ, 0 Ç 0 Other;

Query Match: DB: Percent Similarity: Best Local Similarity: Alignment Scores: No.: 6.79e-60 610.00 100.00% 100.00% 100.00% Gaps: Mismatches: Indels: Conservative: 127 0 0

US-09-017-715A-2 (1-127) x ABL63343 (1-550)

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372 GAGGCCCAGAGTGGGGGAGAC 392	121 GluAlaGlnSerGlyGlyAsp 127	312 AGGCCATCTGCCCCCCAACAGGAGGGTGAGGCATCCAAAGAGAAGAAGAAGAAGTGGCAGAG 371	101 ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluCyalAlaGlu 120	252 ACCGTGGAGGAGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG 311	81 ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu 100	192 GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG 251	61 GluGlnAlaAsnAlaValSerLysAlaValValSerSerValAsnThrValAlaThrLys 80	132 GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG 191	41 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys 60	72 AAGACCAAGCAGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGGGTCATGTATGT	21 LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal 40	12 ATGGATGTTTTCAAGAAGGGCTTCTCCATCGCCAAGAAGGGCGTGGTGGGTG	1 MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 20

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RESULT 4
ABV73813
ID ABV7
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XX ABV7
XX ABV7
XX Gamm
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XX Gamm
XX Homc
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                                                                                                                                                                          The present sequence is that of cDNA encoding the Glu-110 isoform of CC human gamma-synuclein. The invention relates to an isoform of gamma-CC synuclein that is caused by an A/T single nucleotide polymorphism (SNP) CC at position 329 of the gamma-synuclein coding sequence. This SNP causes a CC glutamic acid to valine change at amino acid position 110 of gamma-CC synuclein, and is associated with an increased susceptibility of CC individuals to schizophrenia spectrum disorders (SSDs). This is the first CC time that a genetic component of SSDs has been identified, and provides a component of synuclein polypeptides, especially those containing the EllOV mutation, CC are used in a claimed method of screening for compounds useful for the treatment of SSDs, and gamma-synuclein expressing cells are used in a CC claimed method of screening for agonist or antagonist compounds. An CC claimed method of screening for agonist or antagonist compounds. An CC claimed method of screening for agonist or antagonist compounds. Of sequence is used for the discrimination of an SNP at position 329 of the CC coding sequence. Gamma-synuclein polypeptides or polynucleotides are also useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR camplification of a polynucleotide encoding gamma-synuclein and analysis of the occurrence of the SNP at position 329. A transgenic animal useful control of the StDs is also claimed
   Score:
                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for compounds for treating or interfering with the onset Schizophrenia Spectrum Disorders, by detecting interactions of came compounds with the gamma-synuclein polypeptide.
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                                                                                                                            Sequence 550 BP; 132 A; 145 C;
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NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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/transl_except= (pos:213. .215,aa:Glu)
replace(340,T)
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12. .395
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6.79e-60
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                                                                                                                            192 G; 81
Length:
Matches:
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New isolated protein and nucleic acid molecules, useful for diagnostic and therapeutic purposes, e.g. for treating genetic diseases such as {\sf acid}
                                                                                                                                                                                                                                                         30-AUG-1995;
30-AUG-1996;
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                                                                               P-PSDB; ABW02024.
                                                                                                       WPI; 2003-842790/78
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                                                                                                                                                            PA;
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96US-00705771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human amyloid-like protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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RRESULT 6
ADG47636
ID ADG47
XX ADG4
AC ADG4
XX ADG4
XX Huma
XX Huma
XX Huma
XX Bs;
KW Bs;
KW Bs;
KW OSTE
XX OS Homc
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                                                                                ss; gene; muscular dystrophy; cystic fibrosis; hypertension;
angina pectoris; myocardial infarction; ulcer; asthma; allergy;
psychosis; depression; migraine; vomiting; benign prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated new isolated protein and nucleic act molecules useful for diagnostic and therapeutic purposes. The inventic is for treating genetic diseases such as muscular dystrophy or cystic fibrosis, and for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors. The invention is usef in gene therapy. The present sequence is human amyloid-like protein of
                                                                                                                                           11-MAR-2004
                                                                                                                                                                                ADG47636 standard;
                                                                                                                        Human
                                                                                                                                                              ADG47636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 550 BP;
                                                       Homo
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                                                                                                                                                                                                                                                                                              ACCGTGGAGGAGGAGAACATCGCGGTCACCTCCGGGGTGCTGCGCAAGGAGGACTTG
                                                                                                                                                                                                                                                                                                         ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu
                                                                                                                                                                                                                                                                                                                                   GAGCAGGCCAACGCCGTGAGCAAGGCTGTGGTGAGCAGCGTCAACACTGTGGCCACCAAG
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                                                                                                                                                                                                                                                                                                                                                                          GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG
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        /*tag= a
/product= "Amyloid like
                                   Location/Qualifiers
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30-AUG-1996;
14-OCT-1999;
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P-PSDB; ADG47647.
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                         GluAlaGlnSerGlyGlyAsp
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96US-00705771.
99US-00417540.
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New human polypeptides and polynucleotides, useful for diagnosing or treating genetic diseases such as muscular dystrophy or cystic fibrosis, hypertension, asthma, depression or osteoporosis. Claim 18; SEQ ID NO 1; 56pp; English.

The invention relates to an isolated human polypeptide. The polypeptides, polynucleotides, agonists or antagonist are useful for diagnosing or treating genetic diseases such as muscular dystrophy or cystic fibrosis, hypertension, angina pectoris, myocardial infarction, ulcers, asthma, allergies, psychoses, depression, migraine, vomiting, benign prostatic hypertrophy or osteoporosis. The polypeptides and polynucleotides are useful for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vector. The present sequence represents cDNA encoding human amyloid like protein.

192 G; 81 T; 0 ä 0

DB:	Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
10	100.00%	100.00%	100.00%	610.00	6.79e-60	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
0	0	0	0	127	550	

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RESULT 7
ABV73915
ID ABV7
XX ABV7
XX ABV7
XX ABV7
XX Gamm
KW Gamm
KW Schil
XX Homc
XX 
                                                                                     CC human gamma-synuclein. The invention relates to an isoform of gamma-
CC synuclein that is caused by an A/T single nucleotide polymorphism (SNP)
CC at position 329 of the gamma-synuclein coding sequence. This SNP causes a
CC glutamic acid to valine change at amino acid position 110 of gamma-
CC synuclein, and is associated with an increased susceptibility of
CC individuals to schizophrenia spectrum disorders (SSDs). This is the first
CC time that a genetic component of SSDs has been identified, and provides a
CC potential target for diagnosis and treatment of schizophrenia. Gamma-
CC synuclein polypeptides, especially those containing the EllOV mutation,
CC are used in a claimed method of screening for compounds useful for the
CC treatment of SSDs, and gamma-synuclein expressing cells are used in a
CC claimed method of screening for agonist or antagonist compounds. An
CC claimed method of screening for agonist or antagonist compounds
CC sequence is used for the discrimination of an SNP at position 329 of the
CC coding sequence. Gamma-synuclein polypeptides or polynucleotides are also
CC useful for the diagnosis of SSDs, or susceptibility to SSDs, e.g. by PCR
CC amplification of a polynucleotide encoding gamma-synuclein and analysis
CC of the occurrence of the SNP at position 329. A transgenic animal useful
CC shown in the specification but is derived from the gamma-synuclein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for compounds for treating or interfering with the onset of Schizophrenia Spectrum Disorders, by detecting interactions of candidate compounds with the gamma-synuclein polypeptide.
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schizophrenia; neuroleptic;
Sequence 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of cDNA encoding the Val-110 isoform
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)B; ABP54933.
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                                                                given in Fig 1 (see ABV73813)
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/transl_except= (pos:213. .215,aa:Glu)
replace(340,A)
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tic; mutant; gene; ss.
145 C; 192 G; 82 T;
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Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO 13838.
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                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                 P-PSDB; AAO13847
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nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                           Human breast
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                                                                                                                                                                                                                                         Human; breast cancer; ovarian cancer; cytostatic;
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                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                   CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB59718 - AAB59728. The DNA and protein sequences are CC associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention. The breast and ovarian cancer associated DNA, protein, agonist CC invention. The breast and ovarian cancer associated DNA, protein, agonist CC antigonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; CC antiinflammatory; antilcer; vulnerary; anticonvulsant; antidiabetic; CC antiingal; antiparasitic and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists CC and agonists may also be used in the diagnosis, prevention and treatment CC immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; inference in a ference of inference such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                        Sequence 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatmen and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611515/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 608; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological diseases.
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                                                                        This invention relates to a novel method for identifying genes that are cover-expressed in adipose tissue and as such it provides targets for anti co-besity pharmaceutical compositions. Specifically, it refers to a high can mobility group I-C protein (HMGI-C) that is associated with obesity and can expressive trait is linked to obesity and diabetes. The present composition are expression analysis of invention describes performing differential gene expression analysis of the white adipose tissue (WAT) or strongly varied that result (WT) composition or strongly using confident mice selected from a group consisting of wild-type, composition and candiovascular specific, and as such can be used for preventing adipogenesis, diagnosing and treating diabetes obesity, these compositions exhibit anorecitic, antidiabetes or obesity. These compositions exhibit anorecitic, antidiabetes a human homologue of a murine adipocyte specific DNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying adipocyte specific genes, useful for treating obesity or diabetes, and for identifying drug targets, by differential gene expression analysis between adipose tissue or stromal vascular tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; adipocyte specific; gene; ds; adipose tissue; anti-obesity; high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes; adipogenesis; hypertension; cardiovascular disease; anorectic; antidiabetic; hypotensive; gamma synuclein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 20; 91pp; English.
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Sequence 488 BP; 127 A; 119 C; 176 G; 66 T; 0 U; 0 Other;

Claim 29; Page 16-17; 39pp; English

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
RESULT 11
AAX299
XX AAX29
XX DAX29
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                                New synuclein protein (persyn) and gene, useful in assays for screening, diagnosing or monitoring cancer, neurodegenerative disorders or skin
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                                                                                                                                                                                                                                                                    Human; synuclein;
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intermediate filament damage; ss.
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                                                                                                                                                      Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the gene encoding a novel human synuclein family member designated persyn. The sequence is useful for screening, diagnosing or monitoring cancer (especially breast or skin cancer), neurodegenerative disorders or skin disorders and for identifying cells having intermediate filament damage
                                                                                                                nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
             14-MAR-2002; 2002WO-US007826
                                                                                                                                                                                                                       cDNA encoding
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CC patient is afflicted with ovarian cancer. The method involves comparing CC the expression level of a marker in a patient sample and the normal level CC of expression of the marker in a control non-ovarian cancer sample, where CC the marker is selected from 363 cancer markers described in the CC specification. The method of the invention is useful in diagnosing or CC characterising cancer, in detecting the presence of cancer as early as CC possible, and the recurrence of ovarian cancer. The method may also be of CC particular use with patients having an enhanced risk of developing CC ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment CC of e.g. brain and central nervous system disorders (e.g. bacterial and CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain (CC disorders (e.g. bacterial or viral meningitis or encephalitis), CC inflammations (e.g. bacterial or viral meningitis or encephalitis), CC connective tissue disorders, or heart disorders (e.g. ischaemic heart CC disease or atherosclerosis). The compositions and methods may also be CC used in assessing the histological type of neoplasm associated with CC ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2001; 2001US-0276025P.
14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325102P.
Sequence
                                                             selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic sequence encodes one of the ovarian cancer markers described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 411; 481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new method
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Ś 밁 S Percent Similarity: Best Local Similari US-09-017-715A-2 (1-127) x ABS76519 (1-720) No.: Match: Similarity: 21 49  $\vdash$ LysThrLysGlnGlyValThrGluAlaAlaGluLysThrLysGluGlyValMetTyrVal MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu 4.82e-58 595.00 99.21% 97.64% 97.54% Length: Matches: Conservative: Mismatches: Indels: 720 124 2 1 0

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GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys

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08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
       The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from upa (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulindegrading enzyme), KNSL1 (Kinesin-like protein 1), LIFA (lysosomal acid lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on
                                                                                                                                                                                                                                                                                              Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
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25-OCT-2001; 25-OCT-2001; 02-NOV-2001; 08-NOV-2001; 08-NOV-2001; human; neurodegenerative disease; urokinase plasminogen activator; gamma-synuclein; SNCG; insulin degrading enzyme; IDE; kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA; tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; 04-DEC-2003 US2003224380-A1 Human SNCG 25-MAR-2004 ADH54342; 25-OCT-2002; ADH54342 sapiens standard; gene cDNA sequence SeqID469. ; 2001US-0339525P.; 2001US-0348065P.; 2001US-0336983P.; 2001US-0336983P.; 2001US-0338363P. 2002US-00282174. (first entry) CDNA; 720

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28-MAR-2002;
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GAGGCCCAGAGTGGGGGAGAC
             standard;
                                                                                                                               ArgProSerAlaProGlnGlnGluGlyGluAlaSerLysGluLysGluGluValAlaGlu
                                                                                                                                                                                  ThrValGluGluAlaGluAsnIleAlaValThrSerGlyValValArgLysGluAspLeu
                                                                                                                                                                                                                 GlyAlaLysThrLysGluAsnValValGlnSerValThrSerValAlaGluLysThrLys
                                                                                                                                                                                                                                                                                                                         MetAspValPheLysLysGlyPheSerIleAlaLysLysGlyValValGlyAlaValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ing a predisposition for or the occurrence of neurodegenerative particularly Alzheimer's disease, comprises determining the of a polymorphism in the uPA, SNCG, IDE, KNSLI, LIPA or TNFRSF6
                                                                                                                AGGCCATCTGCCCCCAACAGGAGGGTGNGGCATCCAAAGAGAAAAGAGAAGTGGCAGAG
                                                                                                                                                                  ACCGTGGAGGAGGAGAACATCGCGGTCACCTCCGGGGTGGTGCGCAAGGAGGACTTG
                                                                                                                                                                                                                                                                      GGAGCCAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAG
                                                                                                                                                                                                                                                                                                                                                                           ATGGATGTNTTCAAGAAGGGCTTCTCCATCGCCAAGNAGGGCGTGGTGGGTGCGGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 469; 205pp; English.
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Saunders AJ,
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2002US-0368919P
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97.64%
97.05%
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Mullin KM, Sampson
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Matches:
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Indels:
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                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide comprising any one o 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR,
                                                                                                                                                                                                                                                                   for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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(STAC/)
(DICK/)
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                                                                 12 LysLysGlyValValGlyAlaValGluLysThrLysGlnGlyValThrGluAlaAlaGlu
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JONES L W.
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           LysThrLysGluGlyValMetTyrValGlyAlaLysThrLysGluAsnValValGlnSer
                                                     CAGGAGGGCGTGGNGGGTGCGGTGGAAAAGACCAAGCAGGGGGT
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ping; biodiversity; genetic disorder.
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Search Job ti	Ф	ş	Дb	ş	дb	Ş	đđ	Ş
Search completed: May 4, 2005, 09:26:16 Job time : 934.208 secs	347 TCCAAAGAGAAAGAGTGGCAGAGGCCCAGAGTGGGGGAGAC 394	112 SerLysGluLysGluGluValAlaGluGluAlaGlnSerGlyGlyAsp 127	287 TCCGGGGTGGTGCGCAAGGAGGACTTGAGGCCATCTGCCCCCCAACAGGAGGGTGAGGCA 346	92 SerGlyValValArgLysGluAspLeuArgProSerAlaProGlnGlnGluGlyGluAla 111	227 AGCAGCGTCAACACTGTGGCCACCAAGACCGTGGAGGAGGCGGAGAACATCGCGGTCACC 286	72 SerSerValAsnThrValAlaThrLysThrValGluGluAlaGluAsnIleAlaValThr 91	167 GTGACCTCAGTGGCCGAGAAGACCAAGGAGCAGGCCAACGCCGTGAGCGAGGCTGTGGTG 226	52 ValThrSerValAlaGluLysThrLysGluGlnAlaAsnAlaValSerLysAlaValVal 71